

**Docket No.: 15966-559 CON-S6 (Cura-59 CON-S6)**

jc760 U.S. PRO  
10/004551  
12/05/01

**FOR: Novel Amino Acid Sequences For Human Fetal Brain-like Polypeptides**

**REQUEST FOR TRANSFER OF SEQUENCE LISTING UNDER 37 C.F.R. § 1.821(e)**

A paper copy of the Sequence Listing was included in the originally filed specification of the earliest priority application, application number 09/635,949 filed August 10, 2000. Please use only the paper copy of the Sequence listing of this application as the paper copy for the instant application.

Respectfully submitted,

Dated: December 5, 2001

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Naomi S. Biswas, Reg. No. 38,384  
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Boston, Massachusetts 02111  
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Fax: (617) 542-2241



SEQUENCE LISTING

RECEIVED  
NOV 27 2001  
TECH CENTER 1600/2900

<110> SHIMKETS, RICHARD A  
FERNANDES, ELMA

<120> POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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<141> 2000-08-10

<150> 09/635,949, 8/10/2000

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<151> 1999-08-11

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APR  
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Gly Lys Trp Ser Gly Arg Ala Pro Ser Cys Ile Pro Ile Cys Gly Lys

435	440	445
Ile Glu Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp Pro Trp		
450	455	460
Gln Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly Ser Leu		
465	470	475 480
His Lys Gly Ala Trp Phe Leu Val Cys Ser Gly Ala Leu Val Asn Glu		
485	490	495
Arg Thr Val Val Val Ala Ala His Cys Val Thr Asp Leu Gly Lys Val		
500	505	510
Thr Met Ile Lys Thr Ala Asp Leu Lys Val Val Leu Gly Lys Phe Tyr		
515	520	525
Arg Asp Asp Asp Arg Asp Glu Lys Thr Ile Gln Ser Leu Gln Ile Ser		
530	535	540
Ala Ile Ile Leu His Pro Asn Tyr Asp Pro Ile Leu Leu Asp Ala Asp		
545	550	555 560
Ile Ala Ile Leu Lys Leu Leu Asp Lys Ala Arg Ile Ser Thr Arg Val		
565	570	575
Gln Pro Ile Cys Leu Ala Ala Ser Arg Asp Leu Ser Thr Ser Phe Gln		
580	585	590
Glu Ser His Ile Thr Val Ala Gly Trp Asn Val Leu Ala Asp Val Arg		
595	600	605
Ser Pro Gly Phe Lys Asn Asp Thr Leu Arg Ser Gly Val Val Ser Val		
610	615	620
Val Asp Ser Leu Leu Cys Glu Glu Gln His Glu Asp His Gly Ile Pro		
625	630	635 640
Val Ser Val Thr Asp Asn Met Phe Cys Ala Ser Trp Glu Pro Thr Ala		
645	650	655
Pro Ser Asp Ile Cys Thr Ala Glu Thr Gly Gly Ile Ala Ala Val Ser		
660	665	670
Phe Pro Gly Arg Ala Ser Pro Glu Pro Arg Trp His Leu Met Gly Leu		
675	680	685
Val Ser Trp Ser Tyr Asp Lys Thr Cys Ser His Arg Leu Ser Thr Ala		
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<220>  
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agacggggga gggctattac tccaattcac tgtcaatgga attacagcta tagcggcagt 180  
gtatatagga ttgcttttc tcgtcttctt ggagatgctc agtcccagta tattttaagg 240  
aagagaaata taaaggaaat ttagtatgcc tccttttctt taaatgaaga atttagtttc 300  
cttacttctt taaaagagaa tacctgttct tgtataacgt gactgcacca gacattctga 360  
aaaatcagca agaagcaaaa gctggaaata gctatttcac agcagggttc tgaagtaacg 420  
gaagctacct tgtataaaga cctcaacact gctgacc atg atc agc gca gcc tgg 475  
Met Ile Ser Ala Ala Trp  
1 5

agc atc ttc ctc atc ggg act aaa att ggg ctg ttc ctt caa gta gca 523  
Ser Ile Phe Leu Ile Gly Thr Lys Ile Gly Leu Phe Leu Gln Val Ala  
10 15 20

cct cta tca gtt atg gct aaa tcc tgt cca tct gtg tgt cgc tgc gat 571  
Pro Leu Ser Val Met Ala Lys Ser Cys Pro Ser Val Cys Arg Cys Asp  
25 30 35

gcg ggt ttc att tac tgt aat gat cgc ttt ctg aca tcc att cca aca 619  
Ala Gly Phe Ile Tyr Cys Asn Asp Arg Phe Leu Thr Ser Ile Pro Thr  
40 45 50

gga ata cca gag gat gct aca act ctc tac ctt cag aac aac caa ata 667  
Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr Leu Gln Asn Asn Gln Ile  
55 60 65 70

aat aat gct ggg att cct tca gat ttg aaa aac ttg ctg aaa gta gaa 715  
Asn Asn Ala Gly Ile Pro Ser Asp Leu Lys Asn Leu Leu Lys Val Glu  
75 80 85

aga ata tac cta tac cac aac agt tta gat gaa ttt cct acc aac ctc 763  
Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp Glu Phe Pro Thr Asn Leu  
90 95 100

cca aag tat gta aaa gag tta cat ttg caa gaa aat aac ata agg act 811  
Pro Lys Tyr Val Lys Glu Leu His Leu Gln Glu Asn Asn Ile Arg Thr  
105 110 115

atc act tat gat tca ctt tca aaa att ccc tat ctg gaa gaa tta cat 859  
Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro Tyr Leu Glu Glu Leu His  
120 125 130

tta gat gac aac tct gtc tct gca gtt agc ata gaa gag gga gca ttc 907  
Leu Asp Asp Asn Ser Val Ser Ala Val Ser Ile Glu Glu Gly Ala Phe  
135 140 145 150

cga gac agc aac tat ctc cga ctg ctt ttc ctg tcc cgt aat cac ctt 955  
Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe Leu Ser Arg Asn His Leu  
155 160 165

agc aca att ccc tgg ggt ttg ccc agg act ata gaa gaa cta cgc ttg 1003  
Ser Thr Ile Pro Trp Gly Leu Pro Arg Thr Ile Glu Glu Leu Arg Leu  
170 175 180

gat gat aat cgc ata tcc act att tca tca cca tct ctt caa ggt ctc 1051  
Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser Pro Ser Leu Gln Gly Leu  
185 190 195

act agt cta aaa cgc ctg gtt cta gat gga aac ctg ttg aac aat cat 1099  
Thr Ser Leu Lys Arg Leu Val Leu Asp Gly Asn Leu Leu Asn Asn His  
200 205 210

ggc tta ggt gac aaa gtt ttc ttc aac cta gtt aat ttg aca gag ctg 1147  
Gly Leu Gly Asp Lys Val Phe Phe Asn Leu Val Asn Leu Thr Glu Leu  
215 220 225 230

tcc ctg gtg cgg aat tcc ctg act gct gca cca gta aac ctt cca ggc 1195  
Ser Leu Val Arg Asn Ser Leu Thr Ala Ala Pro Val Asn Leu Pro Gly  
235 240 245

aca aac ctg agg aag ctt tat ctt caa gat aac cac atc aat cgg gtg 1243  
Thr Asn Leu Arg Lys Leu Tyr Leu Gln Asp Asn His Ile Asn Arg Val  
250 255 260

ccc cca aat gct ttt tct tat cta agg cag ctc tat cga ctg gat atg 1291  
Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln Leu Tyr Arg Leu Asp Met  
265 270 275

tcc aat aat aac cta agt aat tta cct cag ggt atc ttt gat gat ttg 1339  
Ser Asn Asn Asn Leu Ser Asn Leu Pro Gln Gly Ile Phe Asp Asp Leu  
280 285 290

gac aat ata aca caa ctg att ctt cgc aac aat ccc tgg tat tgc ggg 1387  
Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn Asn Pro Trp Tyr Cys Gly  
295 300 305 310

tgc aag atg aaa tgg gta cgt gac tgg tta caa tca cta cct gtg aag 1435  
Cys Lys Met Lys Trp Val Arg Asp Trp Leu Gln Ser Leu Pro Val Lys  
315 320 325

gtc aac gtg cgt ggg ctc atg tgc caa gcc cca gaa aag gtt cgt ggg 1483  
Val Asn Val Arg Gly Leu Met Cys Gln Ala Pro Glu Lys Val Arg Gly  
330 335 340

atg gct att aag gat ctc aat gca gaa ctg ttt gat tgt aag gac agt 1531  
Met Ala Ile Lys Asp Leu Asn Ala Glu Leu Phe Asp Cys Lys Asp Ser  
345 350 355

ggg att gta agc acc att cag ata acc act gca ata ccc aac aca gtg 1579  
Gly Ile Val Ser Thr Ile Gln Ile Thr Thr Ala Ile Pro Asn Thr Val  
360 365 370

tat cct gcc caa gga cag tgg cca gct cca gtg acc aaa cag cca gat 1627  
Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro Val Thr Lys Gln Pro Asp  
375 380 385 390

att aag aac ccc aag ctc act aag gat caa caa acc aca ggg agt ccc 1675  
Ile Lys Asn Pro Lys Leu Thr Lys Asp Gln Gln Thr Thr Gly Ser Pro  
395 400 405

tca aga aaa aca att aca att act gtg aag tct gtc acc tct gat acc 1723  
Ser Arg Lys Thr Ile Thr Ile Thr Val Lys Ser Val Thr Ser Asp Thr  
410 415 420

att cat atc tct tgg aaa ctt gct cta cct atg act gct ttg aga ctc 1771  
Ile His Ile Ser Trp Lys Leu Ala Leu Pro Met Thr Ala Leu Arg Leu  
425 430 435

agc tgg ctt aaa ctg ggc cat agc ccg gca ttt gga tct ata aca gaa 1819  
Ser Trp Leu Lys Leu Gly His Ser Pro Ala Phe Gly Ser Ile Thr Glu  
440 445 450

aca att gta aca ggg gaa cgc agt gag tac ttg gtc aca gcc ctg gag 1867  
Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr Leu Val Thr Ala Leu Glu  
455 460 465 470

cct gat tca ccc tat aaa gta tgc atg gtt ccc atg gaa acc agc aac 1915  
Pro Asp Ser Pro Tyr Lys Val Cys Met Val Pro Met Glu Thr Ser Asn  
475 480 485

ctc tac cta ttt gat gaa act cct gtt tgt att gag act gaa act gca 1963  
Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys Ile Glu Thr Glu Thr Ala  
490 495 500

ccc ctt cga atg tac aac cct aca acc acc ctc aat cga gag caa gag 2011  
Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr Leu Asn Arg Glu Gln Glu  
505 510 515

aaa gaa cct tac aaa aac ccc aat tta cct ttg gct gcc atc att ggt 2059



Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro Leu Ala Ala Ile Ile Gly  
520 525 530

ggg gct gtg gcc ctg gtt acc att gcc ctt ctt gct tta gtg tgt tgg 2107  
Gly Ala Val Ala Leu Val Thr Ile Ala Leu Leu Ala Leu Val Cys Trp  
535 540 545 550

tat gtt cat agg aat gga tct ctc ttc tca agg aac tgt gca tat agc 2155  
Tyr Val His Arg Asn Gly Ser Leu Phe Ser Arg Asn Cys Ala Tyr Ser  
555 560 565

aaa ggg agg aga aga aag gat gac tat gca gaa gct ggc act aag aag 2203  
Lys Gly Arg Arg Lys Asp Asp Tyr Ala Glu Ala Gly Thr Lys Lys  
570 575 580

gac aac tct atc ctg gaa atc agg gaa act tct ttt cag atg tta cca 2251  
Asp Asn Ser Ile Leu Glu Ile Arg Glu Thr Ser Phe Gln Met Leu Pro  
585 590 595

ata agc aat gaa ccc atc tct aag gag gag ttt gta ata cac acc ata 2299  
Ile Ser Asn Glu Pro Ile Ser Lys Glu Glu Phe Val Ile His Thr Ile  
600 605 610

ttt cct cct aat gga atg aat ctg tac aaa aac aat cac agt gaa agc 2347  
Phe Pro Pro Asn Gly Met Asn Leu Tyr Lys Asn Asn His Ser Glu Ser  
615 620 625 630

agt agt aac cga agc tac aga gac agt ggt att cca gac tca gat cac 2395  
Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly Ile Pro Asp Ser Asp His  
635 640 645

tca cac tca tgatgctgaa ggactcacag cagactgtg ttttgggttt 2444  
Ser His Ser

tttaaaccta agggagggtga tggtaggaac cctgttctac tgcaaaacac tggaaaaaga 2504

gactgaaaaa aagcaatgta ctgtacattt gccatataat ttatatataa gaacttttta 2564

ttaaaagttt caaatttcag gttactgctg cgattgatgt agtggagatg cctgaacaca 2624

attctatatt ttagtatttt ttagtaattt gtactgtatt ttcttgcaa atattggagt 2684

tataaaccat ttactttgtg ttctactgag taagatgact tgttgactgt gaaagtgaat 2744

tttcttgctg tgtcgaacaa tcaggactgc attcatatga gatccttgta gtataagcac 2804

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<211> 649

<212> PRT

<213> Homo sapiens

<400> 6

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Leu Phe Leu Gln Val Ala Pro Leu Ser Val Met Ala Lys Ser Cys Pro

20 25 30

Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Phe

35 40 45

Leu Thr Ser Ile Pro Thr Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr

50 55 60

Leu Gln Asn Asn Gln Ile Asn Asn Ala Gly Ile Pro Ser Asp Leu Lys

65 70 75 80

Asn Leu Leu Lys Val Glu Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp

85 90 95

Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His Leu Gln

100 105 110

Glu Asn Asn Ile Arg Thr Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro

115 120 125

Tyr Leu Glu Glu Leu His Leu Asp Asp Asn Ser Val Ser Ala Val Ser

130 135 140

Ile Glu Glu Gly Ala Phe Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe

145 150 155 160

Leu Ser Arg Asn His Leu Ser Thr Ile Pro Trp Gly Leu Pro Arg Thr

165 170 175

Ile Glu Glu Leu Arg Leu Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser

180 185 190

Pro Ser Leu Gln Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp Gly

195 200 205

Asn Leu Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn Leu

210 215 220

Val Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala Ala

225 230 235 240

Pro Val Asn Leu Pro Gly Thr Asn Leu Arg Lys Leu Tyr Leu Gln Asp

245 250 255

Asn His Ile Asn Arg Val Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln

260 265 270

Leu Tyr Arg Leu Asp Met Ser Asn Asn Leu Ser Asn Leu Pro Gln  
275 280 285

Gly Ile Phe Asp Asp Leu Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn  
290 295 300

Asn Pro Trp Tyr Cys Gly Cys Lys Met Lys Trp Val Arg Asp Trp Leu  
305 310 315 320

Gln Ser Leu Pro Val Lys Val Asn Val Arg Gly Leu Met Cys Gln Ala  
325 330 335

Pro Glu Lys Val Arg Gly Met Ala Ile Lys Asp Leu Asn Ala Glu Leu  
340 345 350

Phe Asp Cys Lys Asp Ser Gly Ile Val Ser Thr Ile Gln Ile Thr Thr  
355 360 365

Ala Ile Pro Asn Thr Val Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro  
370 375 380

Val Thr Lys Gln Pro Asp Ile Lys Asn Pro Lys Leu Thr Lys Asp Gln  
385 390 395 400

Gln Thr Thr Gly Ser Pro Ser Arg Lys Thr Ile Thr Ile Thr Val Lys  
405 410 415

Ser Val Thr Ser Asp Thr Ile His Ile Ser Trp Lys Leu Ala Leu Pro  
420 425 430

Met Thr Ala Leu Arg Leu Ser Trp Leu Lys Leu Gly His Ser Pro Ala  
435 440 445

Phe Gly Ser Ile Thr Glu Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr  
450 455 460

Leu Val Thr Ala Leu Glu Pro Asp Ser Pro Tyr Lys Val Cys Met Val  
465 470 475 480

Pro Met Glu Thr Ser Asn Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys  
485 490 495

Ile Glu Thr Glu Thr Ala Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr  
500 505 510

Leu Asn Arg Glu Gln Glu Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro  
515 520 525

Leu Ala Ala Ile Ile Gly Gly Ala Val Ala Leu Val Thr Ile Ala Leu  
530 535 540

Leu Ala Leu Val Cys Trp Tyr Val His Arg Asn Gly Ser Leu Phe Ser  
545 550 555 560

Arg Asn Cys Ala Tyr Ser Lys Gly Arg Arg Arg Lys Asp Asp Tyr Ala  
565 570 575

Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu Glu Ile Arg Glu Thr  
580 585 590

Ser Phe Gln Met Leu Pro Ile Ser Asn Glu Pro Ile Ser Lys Glu Glu  
595 600 605

Phe Val Ile His Thr Ile Phe Pro Pro Asn Gly Met Asn Leu Tyr Lys  
610 615 620

Asn Asn His Ser Glu Ser Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly  
625 630 635 640

Ile Pro Asp Ser Asp His Ser His Ser  
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<210> 7

<211> 1653

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (964)..(1443)

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aagacatttg tgttttacac acataaggat ctgtgttttg ggtttctct tctcccctg 180

acattggcat tgcttagtgg ttgtgtggg agggagacca cgtgggctca gtgcttgctt 240

gcacttatct gcctaggtac atcgaagtct ttgacctcc atacagtgat tatgcctgtc 300

atcgctggtg gtatcctggc ggccttgctc ctgctgatag ttgtctgtct ctgtctttac 360

ttcaaaatac acaacgcgtc aaaagctgca aaggaaacctg aagctgtggc tgtaaaaaat 420

cacaaccag acaagggtgtg gtgggccaag aacagccagg ccaaaccat tgccacggag 480

tctgtcctg cctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540

ccacctgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaa 600

gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660

agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720  
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 ctcacacaaa tctacccctt gcgtggctgg aactgacgtt tccttgagg tgtccagaaa 900  
 gctgatgtaa cacagagcct ataaaagctg tcggtccta aggctgccca gcgccttgcc 960  
 aaa atg gag ctt gta aga agg ctc atg cca ttg acc ctc tta att ctc 1008  
 Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu  
 1 5 10 15  
 tcc tgt ttg gcg gag ctg aca atg gcg gag gct gaa ggc aat gca agc 1056  
 Ser Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser  
 20 25 30  
 tgc aca gtc agt cta ggg ggt gcc aat atg gca gag acc cac aaa gcc 1104  
 Cys Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala  
 35 40 45  
 atg atc ctg caa ctc aat ccc agt gag aac tgc acc tgg aca ata gaa 1152  
 Met Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu  
 50 55 60  
 aga cca gaa aac aaa agc atc aga att atc ttt tcc tat gtc cag ctt 1200  
 Arg Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu  
 65 70 75  
 gat cca gat gga agc tgt gaa agt gaa aac att aaa gtc ttt gac gga 1248  
 Asp Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly  
 80 85 90 95  
 acc tcc agc aat ggg cct ctg cta ggg caa gtc tgc agt aaa aac gac 1296  
 Thr Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp  
 100 105 110  
 tat gtt cct gta ttt gaa tca tca tcc agt aca ttg acg ttt caa ata 1344  
 Tyr Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile  
 115 120 125  
 gtt act gac tca gca aga att caa aga act gtc ttt gtc ttc tac tac 1392  
 Val Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr  
 130 135 140  
 ttc ttc tct cct aac atc tgg ctc tgc att cac agc acc tac att cca 1440  
 Phe Phe Ser Pro Asn Ile Trp Leu Cys Ile His Ser Thr Tyr Ile Pro  
 145 150 155  
 ctg tgatccgaag cagaatgcc aagaacatctg cgagtgggtt catgaggaga 1493  
 Leu  
 160

gctccactgt ggattcttt ccaaggcca gagctgacca tgcactctc ctgtaaac 1553  
cactgacttc ttgtaccag cagatctcca gagtcagca gtcaagggtt tcccacgctg 1613  
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<211> 160  
<212> PRT  
<213> Homo sapiens

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Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Gly Asn Ala Ser Cys  
20 25 30  
Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
35 40 45  
Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
50 55 60  
Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
65 70 75 80  
Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
85 90 95  
Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
100 105 110  
Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
115 120 125  
Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
130 135 140  
Phe Ser Pro Asn Ile Trp Leu Cys Ile His Ser Thr Tyr Ile Pro Leu  
145 150 155 160

<210> 9  
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<212> DNA  
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<220>  
<221> CDS

<222> (273)..(2012)

<400> 9

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aggtgtcttc tctgagaag aactgtccat accatgggtg tggtaggct ttcaccagtt 180

ctcaggatgc ccatagggat gggtaagcc tgcctggcct gtggtgcttt ccagtggccg 240

tcattctatt agggcccccac agtggcatta gg atg cac ctc tcg gcg gtg ttc 293

Met His Leu Ser Ala Val Phe

1 5

aac gcc ctc ctg gtg tcg gtg ctg gca gcg gtc ctg tgg aag cat gtg 341

Asn Ala Leu Leu Val Ser Val Leu Ala Ala Val Leu Trp Lys His Val

10 15 20

cgg ctg cgt gag cat gca gcc aca ctg gag gag gag ctg gcc ctc agc 389

Arg Leu Arg Glu His Ala Ala Thr Leu Glu Glu Glu Leu Ala Leu Ser

25 30 35

cga cag gcc aca gag cca gcc cca gca ctg agg atc gac tac ccg aag 437

Arg Gln Ala Thr Glu Pro Ala Pro Ala Leu Arg Ile Asp Tyr Pro Lys

40 45 50 55

gca ctg cag atc ctg atg gag ggc ggc aca cac atg gtg tgc acg ggc 485

Ala Leu Gln Ile Leu Met Glu Gly Gly Thr His Met Val Cys Thr Gly

60 65 70

cgc acg cac aca gac cgc atc tgc cgc ttc aag tgg ctc tgc tac tcc 533

Arg Thr His Thr Asp Arg Ile Cys Arg Phe Lys Trp Leu Cys Tyr Ser

75 80 85

aac gag gct gag gag ttc atc ttc ttc cat ggc aac acc tct gtc atg 581

Asn Glu Ala Glu Glu Phe Ile Phe Phe His Gly Asn Thr Ser Val Met

90 95 100

ctg ccc aac ctg ggc tcc cgg cgc ttc cag cca gcc ctg ctc gac cta 629

Leu Pro Asn Leu Gly Ser Arg Arg Phe Gln Pro Ala Leu Leu Asp Leu

105 110 115

tcc acc gtg gag gac cac aac act cag tac ttc aac ttc gtg gag ctg 677

Ser Thr Val Glu Asp His Asn Thr Gln Tyr Phe Asn Phe Val Glu Leu

120 125 130 135

cct gct gct gcc ctg cgc ttc atg ccc aag ccg gtg ttc gtg cca gac 725

Pro Ala Ala Ala Leu Arg Phe Met Pro Lys Pro Val Phe Val Pro Asp

140 145 150

gtg gcc ctc atc gcc aac cgc ttc aac ccc gac aac ctc atg cac gtc 773

Val Ala Leu Ile Ala Asn Arg Phe Asn Pro Asp Asn Leu Met His Val

155	160	165
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ggc ctg gcc cac gag gca cgg ctc ttc atg gag ggc tgg ggc gag 869 Gly Leu Ala His Glu Ala Arg Leu Phe Phe Met Glu Gly Trp Gly Glu 185 190 195		
ggt gca cac ttc gac ctc tac aag ctg ctc agc ccc aag cag cct ctc 917 Gly Ala His Phe Asp Leu Tyr Lys Leu Leu Ser Pro Lys Gln Pro Leu 200 205 210 215		
ctg cgg gca cag ctg aag acc ctg ggc cgg ctg ctg tgc ttc tcc cat 965 Leu Arg Ala Gln Leu Lys Thr Leu Gly Arg Leu Leu Cys Phe Ser His 220 225 230		
gct ttt gtg ggc ctc tcc aag atc act acc tgg tac cag tat ggc ttt 1013 Ala Phe Val Gly Leu Ser Lys Ile Thr Thr Trp Tyr Gln Tyr Gly Phe 235 240 245		
gtg cag ccc cag ggc ccg aag gcc aac atc ctc gtc tca ggc aat gag 1061 Val Gln Pro Gln Gly Pro Lys Ala Asn Ile Leu Val Ser Gly Asn Glu 250 255 260		
atc cgg cag ttt gca cgg ttc atg aca gaa aag ctg aac gtg agc cac 1109 Ile Arg Gln Phe Ala Arg Phe Met Thr Glu Lys Leu Asn Val Ser His 265 270 275		
aca gga gtc ccc cta ggc gag gag tac att ctg gtc ttt agc cga acc 1157 Thr Gly Val Pro Leu Gly Glu Glu Tyr Ile Leu Val Phe Ser Arg Thr 280 285 290 295		
cag aac aga ctc att ctg aat gag gca gag ctg ctg ctg gca ctg gcc 1205 Gln Asn Arg Leu Ile Leu Asn Glu Ala Glu Leu Leu Leu Ala Leu Ala 300 305 310		
cag gag ttc cag atg aag aca gtg aca gtg tcc ctg gag gac cac acc 1253 Gln Glu Phe Gln Met Lys Thr Val Thr Val Ser Leu Glu Asp His Thr 315 320 325		
ttt gct gat gtc gtg cgg ctg gtc agc aat gcc tcc atg ctg gtc agc 1301 Phe Ala Asp Val Val Arg Leu Val Ser Asn Ala Ser Met Leu Val Ser 330 335 340		
atg cat ggg gcc cag ctg gtc acc acc ctc ttc ctg ccc cgt ggg gca 1349 Met His Gly Ala Gln Leu Val Thr Thr Leu Phe Leu Pro Arg Gly Ala 345 350 355		
act gtg gta gag ctc ttc cca tat gct gtc aat ccc gac cac tac act 1397 Thr Val Val Glu Leu Phe Pro Tyr Ala Val Asn Pro Asp His Tyr Thr 360 365 370 375		



ccc tat aag acg ctg gcc atg ctg cct ggc atg gac ctc cag tat gta 1445  
 Pro Tyr Lys Thr Leu Ala Met Leu Pro Gly Met Asp Leu Gln Tyr Val  
           380              385              390

gcc tgg cgg aac atg atg cca gag aac aca gtc aca cac cct gag cgg 1493  
 Ala Trp Arg Asn Met Met Pro Glu Asn Thr Val Thr His Pro Glu Arg  
           395              400              405

ccc tgg gat cag ggg ggc atc acc cat ctg gac cgg gct gag caa gcc 1541  
 Pro Trp Asp Gln Gly Gly Ile Thr His Leu Asp Arg Ala Glu Gln Ala  
           410              415              420

cgt atc ctg caa agc cgt gag gtc cca cgg cat ctc tgt tgc cgg aac 1589  
 Arg Ile Leu Gln Ser Arg Glu Val Pro Arg His Leu Cys Cys Arg Asn  
           425              430              435

ccc gag tgg ctc ttc cga atc tac cag gac acc aag gtg gac atc cca 1637  
 Pro Glu Trp Leu Phe Arg Ile Tyr Gln Asp Thr Lys Val Asp Ile Pro  
           440              445              450              455

tcc ctc att caa acc ata cgg cgc gtg gtg aag ggc cgg cca gga cca 1685  
 Ser Leu Ile Gln Thr Ile Arg Arg Val Val Lys Gly Arg Pro Gly Pro  
           460              465              470

cgg aag cag aag tgg aca gtc ggc cta tat cca ggc aag gtg cgg gag 1733  
 Arg Lys Gln Lys Trp Thr Val Gly Leu Tyr Pro Gly Lys Val Arg Glu  
           475              480              485

gca cgg tgc cag gcg tca gtg cat ggc gcc tcc gag gcc cgc ctc act 1781  
 Ala Arg Cys Gln Ala Ser Val His Gly Ala Ser Glu Ala Arg Leu Thr  
           490              495              500

gtc tcc tgg cag atc cca tgg aac ctt aaa tac ctg aag gtg agg gag 1829  
 Val Ser Trp Gln Ile Pro Trp Asn Leu Lys Tyr Leu Lys Val Arg Glu  
           505              510              515

gtg aag tac gag gtg tgg ctg cag gag cag ggg gag aac acc tac gtg 1877  
 Val Lys Tyr Glu Val Trp Leu Gln Glu Gln Gly Glu Asn Thr Tyr Val  
           520              525              530              535

cct tac atc ctg gct ctg cag aac cac acc ttc act gag aac atc aag 1925  
 Pro Tyr Ile Leu Ala Leu Gln Asn His Thr Phe Thr Glu Asn Ile Lys  
           540              545              550

ccc ttc acc acc tac ctg gtg tgg gtc cgc tgc atc ttc aac aag atc 1973  
 Pro Phe Thr Thr Tyr Leu Val Trp Val Arg Cys Ile Phe Asn Lys Ile  
           555              560              565

ctc ctg gga ccc ttt gca gat gtg ctg gtg tgc aac acg tagcgagcag 2022  
 Leu Leu Gly Pro Phe Ala Asp Val Leu Val Cys Asn Thr  
           570              575              580

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 ccactgtgga gacttctggg aactatttat tgagcaggcc tgtgcctcca catcatcttg 2142  
 ttgtctctgg ggtgtggtgt cacagcactc ctcttgccc tagagataag ggacctgact 2202  
 tcccccttc ccatctgaa catttgatcc cctggagaag ttcttagca gggaggagga 2262  
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 ctactgagtt ttctggtat ccagatttct ggaaccgcg taatcatgta ctgtttgatt 2382  
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 Glu Glu Glu Leu Ala Leu Ser Arg Gln Ala Thr Glu Pro Ala Pro Ala  
 35 40 45  
 Leu Arg Ile Asp Tyr Pro Lys Ala Leu Gln Ile Leu Met Glu Gly Gly  
 50 55 60  
 Thr His Met Val Cys Thr Gly Arg Thr His Thr Asp Arg Ile Cys Arg  
 65 70 75 80  
 Phe Lys Trp Leu Cys Tyr Ser Asn Glu Ala Glu Glu Phe Ile Phe Phe  
 85 90 95  
 His Gly Asn Thr Ser Val Met Leu Pro Asn Leu Gly Ser Arg Arg Phe  
 100 105 110  
 Gln Pro Ala Leu Leu Asp Leu Ser Thr Val Glu Asp His Asn Thr Gln  
 115 120 125  
 Tyr Phe Asn Phe Val Glu Leu Pro Ala Ala Ala Leu Arg Phe Met Pro  
 130 135 140  
 Lys Pro Val Phe Val Pro Asp Val Ala Leu Ile Ala Asn Arg Phe Asn  
 145 150 155 160

Pro Asp Asn Leu Met His Val Phe His Asp Asp Leu Leu Pro Leu Phe  
165 170 175

Tyr Thr Leu Arg Gln Phe Pro Gly Leu Ala His Glu Ala Arg Leu Phe  
180 185 190

Phe Met Glu Gly Trp Gly Glu Gly Ala His Phe Asp Leu Tyr Lys Leu  
195 200 205

Leu Ser Pro Lys Gln Pro Leu Leu Arg Ala Gln Leu Lys Thr Leu Gly  
210 215 220

Arg Leu Leu Cys Phe Ser His Ala Phe Val Gly Leu Ser Lys Ile Thr  
225 230 235 240

Thr Trp Tyr Gln Tyr Gly Phe Val Gln Pro Gln Gly Pro Lys Ala Asn  
245 250 255

Ile Leu Val Ser Gly Asn Glu Ile Arg Gln Phe Ala Arg Phe Met Thr  
260 265 270

Glu Lys Leu Asn Val Ser His Thr Gly Val Pro Leu Gly Glu Glu Tyr  
275 280 285

Ile Leu Val Phe Ser Arg Thr Gln Asn Arg Leu Ile Leu Asn Glu Ala  
290 295 300

Glu Leu Leu Leu Ala Leu Ala Gln Glu Phe Gln Met Lys Thr Val Thr  
305 310 315 320

Val Ser Leu Glu Asp His Thr Phe Ala Asp Val Val Arg Leu Val Ser  
325 330 335

Asn Ala Ser Met Leu Val Ser Met His Gly Ala Gln Leu Val Thr Thr  
340 345 350

Leu Phe Leu Pro Arg Gly Ala Thr Val Val Glu Leu Phe Pro Tyr Ala  
355 360 365

Val Asn Pro Asp His Tyr Thr Pro Tyr Lys Thr Leu Ala Met Leu Pro  
370 375 380

Gly Met Asp Leu Gln Tyr Val Ala Trp Arg Asn Met Met Pro Glu Asn  
385 390 395 400

Thr Val Thr His Pro Glu Arg Pro Trp Asp Gln Gly Gly Ile Thr His  
405 410 415

Leu Asp Arg Ala Glu Gln Ala Arg Ile Leu Gln Ser Arg Glu Val Pro  
420 425 430

Arg His Leu Cys Cys Arg Asn Pro Glu Trp Leu Phe Arg Ile Tyr Gln  
435 440 445

Asp Thr Lys Val Asp Ile Pro Ser Leu Ile Gln Thr Ile Arg Arg Val  
450 455 460

Val Lys Gly Arg Pro Gly Pro Arg Lys Gln Lys Trp Thr Val Gly Leu  
465 470 475 480

Tyr Pro Gly Lys Val Arg Glu Ala Arg Cys Gln Ala Ser Val His Gly  
485 490 495

Ala Ser Glu Ala Arg Leu Thr Val Ser Trp Gln Ile Pro Trp Asn Leu  
500 505 510

Lys Tyr Leu Lys Val Arg Glu Val Lys Tyr Glu Val Trp Leu Gln Glu  
515 520 525

Gln Gly Glu Asn Thr Tyr Val Pro Tyr Ile Leu Ala Leu Gln Asn His  
530 535 540

Thr Phe Thr Glu Asn Ile Lys Pro Phe Thr Thr Tyr Leu Val Trp Val  
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Val Cys Asn Thr  
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tgttctcca gacctgggg atg aag gaa aca gga gcc tca ccc agg agg ctc 173  
Met Lys Glu Thr Gly Ala Ser Pro Arg Arg Leu  
1 5 10

aag gcc aaa act ctg acc caa act acc tca gga gcc cct ggc cct ggc 221  
Lys Ala Lys Thr Leu Thr Gln Thr Thr Ser Gly Ala Pro Gly Pro Gly  
15 20 25

ttc ccc cct gct cca gag ttt ctg ccc tgc cca cac aca cac acc ctc 269

Phe Pro Pro Ala Pro Glu Phe Leu Pro Cys Pro His Thr His Thr Leu  
30 35 40

ttc cac cct cag agg ccc cgg tgt cct gcc cca cgc tct acc cca gag 317  
Phe His Pro Gln Arg Pro Arg Cys Pro Ala Pro Arg Ser Thr Pro Glu  
45 50 55

ccc cac ggg tgg ctt tat aaa agt gcc ggg ccc agc cct cta gca gga 365  
Pro His Gly Trp Leu Tyr Lys Ser Ala Gly Pro Ser Pro Leu Ala Gly  
60 65 70 75

ggg gaa tgc tgg gca tct ggg tgt ggg acc ccc ggg gaa cag cct gtg 413  
Gly Glu Cys Trp Ala Ser Gly Cys Gly Thr Pro Gly Glu Gln Pro Val  
80 85 90

gtc tgg act cct gca tct atg agg gga cag acg tgg ctt ccc ttc cgg 461  
Val Trp Thr Pro Ala Ser Met Arg Gly Gln Thr Trp Leu Pro Phe Arg  
95 100 105

atg atg ggg tac cca cag atg atg gag gcc agg gtc cct caa 503  
Met Met Gly Tyr Pro Gln Met Met Glu Ala Arg Val Pro Gln  
110 115 120

taaaagaagg ggtgcaaaaa 523

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35 40 45

Pro Arg Cys Pro Ala Pro Arg Ser Thr Pro Glu Pro His Gly Trp Leu  
50 55 60

Tyr Lys Ser Ala Gly Pro Ser Pro Leu Ala Gly Gly Glu Cys Trp Ala  
65 70 75 80

Ser Gly Cys Gly Thr Pro Gly Glu Gln Pro Val Val Trp Thr Pro Ala  
85 90 95

Ser Met Arg Gly Gln Thr Trp Leu Pro Phe Arg Met Met Gly Tyr Pro  
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Gln Met Met Glu Ala Arg Val Pro Gln  
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caagcccccc gccctccgc cgcggtcca gccaggcg cgccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225  
Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
 115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
 Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
 130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657  
 Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
 145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
 Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
 165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
 Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
 180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
 Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
 195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
 Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
 210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897  
 Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Thr Ile Thr Thr Val Gln Thr  
 225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
 Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
 245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
 Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
 260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
 Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
 275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
 Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
 290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
 Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
 305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
 Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser

325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt caa gct tat gaa gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val  
355 360 365

act gtc acc agc atc cac cca gga ggt agt gcc cgc ttc cat tgt gca 1329  
Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

acc cag ccc atc tgg gat tca aag gag ccc gta tgc atc gct gct tgc 1425  
Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

ggc gga gtg atc cgc aat gcc acc acc ggc cgc atc gtc tct cca ggc 1473  
Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ctg ccc att gag 1665  
Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu  
485 490 495

ggc ctg ctc agc tct ggc aaa cac ttc ttt gtt gag ctc agt act gac 1713  
Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp  
500 505 510

agc agc ggg gca gct gca ggc atg gcc ctg cgc tat gag gcn ttc cag 1761  
Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln  
515 520 525

cag ggc cat tgc tat gag ccc ttt gtc aaa tac ggt aac ttc agc agc 1809  
Gln Gly His Cys Tyr Gly Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser  
530 535 540



agc aca ccc acc tac cct gtg ggt acc act gtg gag ttt agc tgc gac 1857  
Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp  
545 550 555 560

cct ggc tac acc ctg gag cag ggc tcc atc atc atc gag tgt gtt gac 1905  
Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp  
565 570 575

ccc cac gac ccc cag tgg aat gag aca gag cca gcc tgc cga gcc gtg 1953  
Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val  
580 585 590

tgc agc ggg gag atc aca gac tcg gct ggc gtg gta ctc tct ccc aac 2001  
Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn  
595 600 605

tgg cca gag ccc tac agt cgt ggg cag gat tgt atc tgg ggt gtg cat 2049  
Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His  
610 615 620

gtg gaa gag gac aag cgc atc atg ctg gac atc cga gtg ctg cgc ata 2097  
Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile  
625 630 635 640

ggc cct ggt gat gtg ctt acc ttc tat gat ggg gat gac ctg acg gcc 2145  
Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala  
645 650 655

cgg gtt ctg ggc cag tac tca ggg ccc cgt agc cac ttc aag ctc ttt 2193  
Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe  
660 665 670

acc tcc atg gct gat gtc acc att cag ttc cag tcg gac ccc ggg acc 2241  
Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr  
675 680 685

tca gtg ctg ggc tac cag cag ggc ttc gtc atc cac ttc ttt gag gtg 2289  
Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val  
690 695 700

ccc cgc aat gac aca tgt ccg gag ctg cct gag atc ccc aat ggc tgg 2337  
Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp  
705 710 715 720

aag agc cca tcg cag cct gag cta gtg cac ggc acc gtg gtc act tac 2385  
Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr  
725 730 735

cag tgc tac cct ggc tac cag gta gtg gga tcc agt gtc ctc atg tgc 2433  
Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys  
740 745 750

cag tgg gac cta act tgg agt gag gac ctg ccc tca tgc cag agg gtg 2481  
 Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val  
 755 760 765

act tcc tgc cac gat cct gga gat gtg gag cac agc cga cgc ctc ata 2529  
 Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile  
 770 775 780

tcc agc ccc aag ttt ccc gtg ggg gcc acc gtg caa tat atc tgt gac 2577  
 Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp  
 785 790 795 800

cag ggt ttt gtg ctg acg ggc agc tcc atc ctc acc tgc cat gat cgc 2625  
 Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg  
 805 810 815

cag gct ggc agc ccc aag tgg agt gac cgg gcc cct aaa tgt ctc ctg 2673  
 Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu  
 820 825 830

gaa cag ctc aag cca tgc cat ggt ctc agt gcc cct gag aat ggt gcc 2721  
 Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala  
 835 840 845

cga agt cct gag aag cag cta cac cca gca ggg gcc acc atc cac ttc 2769  
 Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe  
 850 855 860

tcg tgt gcc cct ggc tat gtg ctg aag ggc cag gcc agc atc aag tgt 2817  
 Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys  
 865 870 875 880

gtg cct ggg cac ccc tcg cat tgg agt gac ccc cca ccc atc tgt agg 2865  
 Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Pro Ile Cys Arg  
 885 890 895

gct gcc tct ctg gat ggg ttc tac aac agt cgc agc ctg gat gtt gcc 2913  
 Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala  
 900 905 910

aag gca cct gct gcc tcc agc acc ctg gat gct gcc cac att gca gct 2961  
 Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala  
 915 920 925

gcc atc ttc ttg cca ctg gtg gcg atg gtg ttg ttg gta gga ggt gta 3009  
 Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val  
 930 935 940

tac ttc tac ttc tcc agg ctc cag gga aaa agc tcc ctg cag ctg ccc 3057  
 Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro  
 945 950 955 960

cgc ccc cgc ccc cgc ccc tac aac cgc att acc ata gag tca gcg ttt 3105

Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe  
965 970 975

gac aat cca act tac gag act gga gag acg aga gaa tat gaa gtc tcc 3153  
Asp Asn Pro Thr Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser  
980 985 990

atc taggtggggg cagtctaggg aagtcaactc agactgcac cacagtccag 3206  
Ile

cagcaaggct ccttgcttcc tgctgtccct ccacctctg tatataccac ctaggaggag 3266

atgccaccaa gccctcaaga agttgtgccc ttccccgctt gcgatgccca ccatggccta 3326

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<211> 993

<212> PRT

<213> Homo sapiens

<223> n 1755 can be A, G, C, or T

<400> 14

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Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

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Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro

35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu

50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly

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Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro			
85	90	95	
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn			
100	105	110	
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala			
115	120	125	
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser			
130	135	140	
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser			
145	150	155	160
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro			
165	170	175	
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly			
180	185	190	
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile			
195	200	205	
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr			
210	215	220	
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr			
225	230	235	240
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp			
245	250	255	
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe			
260	265	270	
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln			
275	280	285	
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly			
290	295	300	
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly			
305	310	315	320
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser			
325	330	335	
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala			
340	345	350	

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val  
355 360 365

Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu  
485 490 495

Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp  
500 505 510

Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln  
515 520 525

Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser  
530 535 540

Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp  
545 550 555 560

Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp  
565 570 575

Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val  
580 585 590

Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn  
595 600 605

Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His  
610 615 620

Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile  
625 630 635 640

Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala  
645 650 655

Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe  
660 665 670

Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr  
675 680 685

Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val  
690 695 700

Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp  
705 710 715 720

Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr  
725 730 735

Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys  
740 745 750

Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val  
755 760 765

Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile  
770 775 780

Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp  
785 790 795 800

Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg  
805 810 815

Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu  
820 825 830

Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala  
835 840 845

Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe  
850 855 860

Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys  
865 870 875 880

Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Pro Ile Cys Arg  
885 890 895

Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala  
900 905 910

Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala

915                      920                      925  
 Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val  
 930                      935                      940  
 Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro  
 945                      950                      955                      960  
 Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe  
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 Ile

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 caagcccccc gccctccgcg cgcggtccca gccaggggcg cgcccgcaac cagcacc 177  
 atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225  
 Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
 1                      5                      10                      15  
 gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
 Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
 20                      25                      30  
 cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
 Pro Gly Ile Glu Glu Thr Asp Gly Leu Thr Ala Ala Pro Thr Pro  
 35                      40                      45  
 gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
 Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
 50                      55                      60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561  
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Thr Thr Val Gln Thr  
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270



ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt caa gct tat gaa gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val  
355 360 365

act gtc acc agc atc cac cca gga ggt agt gcc cgc ttc cat tgt gca 1329  
Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

acc cag ccc atc tgg gat tca aag gag ccc gta tgc atc gct gct tgc 1425  
Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

ggc gga gtg atc cgc aat gcc acc acc ggc cgc atc gtc tct cca ggc 1473  
Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
Ala Glu Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ctg ccc att gag 1665

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu  
485 490 495

ggc ctg ctc agc tct ggc aaa cac ttc ttt gtt gag ctc agt act gac 1713  
Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp  
500 505 510

agc agc ggg gca gct gca ggc atg gcc ctg cgc tat gag gcn ttc cag 1761  
Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln  
515 520 525

cag ggc cat tgc tat gag ccc ttt gtc aaa tac ggt aac ttc agc agc 1809  
Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser  
530 535 540

agc aca ccc acc tac cct gtg ggt acc act gtg gag ttt agc tgc gac 1857  
Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp  
545 550 555 560

cct ggc tac acc ctg gag cag ggc tcc atc atc atc gag tgt gtt gac 1905  
Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp  
565 570 575

ccc cac gac ccc cag tgg aat gag aca gag cca gcc tgc cga gcc gtg 1953  
Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val  
580 585 590

tgc agc ggg gag atc aca gac tgc gct ggc gtg gta ctc tct ccc aac 2001  
Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn  
595 600 605

tgg cca gag ccc tac agt cgt ggg cag gat tgt atc tgg ggt gtg cat 2049  
Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His  
610 615 620

gtg gaa gag gac aag cgc atc atg ctg gac atc cga gtg ctg cgc ata 2097  
Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile  
625 630 635 640

ggc cct ggt gat gtg ctt acc ttc tat gat ggg gat gac ctg acg gcc 2145  
Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala  
645 650 655

cgg gtt ctg ggc cag tac tca ggg ccc cgt agc cac ttc aag ctc ttt 2193  
Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe  
660 665 670

acc tcc atg gct gat gtc acc att cag ttc cag tgc gac ccc ggg acc 2241  
Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr  
675 680 685

tca gtg ctg ggc tac cag cag ggc ttc gtc atc cac ttc ttt gag gtg 2289  
Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val

690

695

700

ccc cgc aat gac aca tgt ccg gag ctg cct gag atc ccc aat ggc tgg 2337  
 Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp  
 705 710 715 720

aag agc cca tcg cag cct gag cta gtg cac ggc acc gtg gtc act tac 2385  
 Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr  
 725 730 735

cag tgc tac cct ggc tac cag gta gtg gga tcc agt gtc ctc atg tgc 2433  
 Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys  
 740 745 750

cag tgg gac cta act tgg agt gag gac ctg ccc tca tgc cag agg gtg 2481  
 Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val  
 755 760 765

act tcc tgc cac gat cct gga gat gtg gag cac agc cga cgc ctc ata 2529  
 Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile  
 770 775 780

tcc agc ccc aag ttt ccc gtg ggg gcc acc gtg caa tat atc tgt gac 2577  
 Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp  
 785 790 795 800

cag ggt ttt gtg ctg acg ggc agc tcc atc ctc acc tgc cat gat cgc 2625  
 Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg  
 805 810 815

cag gct ggc agc ccc aag tgg agt gac cgg gcc cct aaa tgt ctc ctg 2673  
 Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu  
 820 825 830

gaa cag ctc aag cca tgc cat ggt ctc agt gcc cct gag aat ggt gcc 2721  
 Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala  
 835 840 845

cga agt cct gag aag cag cta cac cca gca ggg gcc acc atc cac ttc 2769  
 Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe  
 850 855 860

tcg tgt gcc cct ggc tat gtg ctg aag ggc cag gcc agc atc aag tgt 2817  
 Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys  
 865 870 875 880

gtg cct ggg cac ccc tcg cat tgg agt gac ccc cca ccc atc tgt agg 2865  
 Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Pro Ile Cys Arg  
 885 890 895

gct gcc tct ctg gat ggg ttc tac aac agt cgc agc ctg gat gtt gcc 2913  
 Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala  
 900 905 910

aag gca cct gct gcc tcc agc acc ctg gat gct gcc cac att gca gct 2961  
Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala

915 920 925

gcc atc ttc ttg cca ctg gtg gcg atg gtg ttg ttg gta gga ggt gta 3009  
Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val

930 935 940

tac ttc tac ttc tcc agg ctc cag gga aaa agc tcc ctg cag ctg ccc 3057  
Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro

945 950 955 960

cgc ccc cgc ccc cgc ccc tac aac cgc att acc ata gag tca gcg ttt 3105  
Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe

965 970 975

gac aat cca act tac gag act gga tct ctt tcc ttt gca gga gac gag 3153  
Asp Asn Pro Thr Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu

980 985 990

aga ata tgaagtctcc atctaggtgg gggcagctca gggaagtcaa ctgagacttg 3209  
Arg Ile

caccagctc cagcagcaag gctccttgct tctgtctgtc cctccacctc ctgtatatac 3269

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ccaccatggc ctatcttctt ggtgtcattg cccacttggg gcccttcatt gggcccatgt 3389

cagggggcat ctacctgtgg gaagaacata gctggagcac aagcatcaac agccagcatc 3449

ctgagcctcc tcatgccctg gaccagctg gaacacacta gcagagcagg agtaccttc 3509

tccacatgac caccatcccg ccttgcatg gcaacctgca gcaggattaa ctgaccatg 3569

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tctaaagttc tggacagltc tgcctctgc cctgtcccag tggaggcagt aattctagga 3749

gatcctaagg gggtcagggg gacctaccc ccacctcagg ttgggcttcc ctgggcactc 3809

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3879

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<211> 994

<212> PRT

<213> Homo sapiens

<223> n 1755 can be A, G, C, or T.

<400> 16

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Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
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Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
 275 280 285

Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
 290 295 300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
 305 310 315 320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
 325 330 335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
 340 345 350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val  
 355 360 365

Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
 370 375 380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
 385 390 395 400

Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
 405 410 415

Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly  
 420 425 430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
 435 440 445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
 450 455 460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
 465 470 475 480

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu  
 485 490 495

Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp  
 500 505 510

Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln  
 515 520 525

Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser  
 530 535 540

Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp

545	550	555	560
Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp			
	565	570	575
Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val			
	580	585	590
Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn			
	595	600	605
Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His			
	610	615	620
Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile			
	625	630	640
Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala			
	645	650	655
Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe			
	660	665	670
Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr			
	675	680	685
Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val			
	690	695	700
Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp			
	705	710	720
Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr			
	725	730	735
Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys			
	740	745	750
Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val			
	755	760	765
Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile			
	770	775	780
Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp			
	785	790	800
Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg			
	805	810	815
Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu			
	820	825	830

Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala  
835 840 845

Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe  
850 855 860

Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys  
865 870 875 880

Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Pro Ile Cys Arg  
885 890 895

Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala  
900 905 910

Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala  
915 920 925

Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val  
930 935 940

Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro  
945 950 955 960

Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe  
965 970 975

Asp Asn Pro Thr Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu  
980 985 990

Arg Ile

<210> 17  
<211> 2127  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (178)..(1752)

<220>  
<223> n 2077 can be A, G, C, or T.

<400> 17  
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ctgcggcccc gctccctcta cccggccgga cccggctctg cccccgcgcc caagccccac 120  
caagcccccc gccctccgc cgcggtccca gccagggcg cgcccgcaac cagcacc 177



atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225  
Met Arg Pro Val Ala Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561  
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val  
355 360 365

act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329  
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425  
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

gcc cca cca gtg gga aaa agc tcc ctg cag ctg ccc cgc ccc cgc ccc 1665  
Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro  
485 490 495

cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713  
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500 505 510

tac gag act gga gag acg aga gaa tat gaa gtc tcc atc tagtggggg 1762  
Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile  
515 520 525

cagctaggg aagtaactc agactgcac cacagtccag cagcaaggct ccttgcttcc 1822

tgctgtccct ccacctctg tatataccac ctaggaggag atgccaccaa gccctcaaga 1882

agttgtgccc ttccccgct gcgatgccca ccatggccta ttttcttggt gtcattgccc 1942

acttggggcc ctgcatgg gccatgtaca gggggcatct acctgtgggg aagaacatag 2002

ctgggagcac aagcttaac agccagcatt ccttgagcct ccttcattggc cctgggacca 2062

gcctggggaa cacanttagg caggagcagg gagttacctt gtttcacatg accaccaacc 2122

attcc 2127

<210> 18

<211> 525

<212> PRT

<213> Homo sapiens

<223> n 2077 can be A, G, C, or T.

<400> 18

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

20	25	30
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro		
35	40	45
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu		
50	55	60
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly		
65	70	75
80		
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro		
85	90	95
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn		
100	105	110
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala		
115	120	125
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser		
130	135	140
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser		
145	150	155
160		
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro		
165	170	175
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly		
180	185	190
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile		
195	200	205
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr		
210	215	220
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr		
225	230	235
240		
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp		
245	250	255
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe		
260	265	270
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln		
275	280	285
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly		
290	295	300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val  
355 360 365

Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro  
485 490 495

Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500 505 510

Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile  
515 520 525

<210> 19

<211> 2127

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (178)..(1752)

<220>

<223> n 2077 can be A, G, C, or T.

<400> 19

ccaggcgctg gccgtggtgc tgattctgtc aggcgtggc gccggcagcg gcggtgacgg 60

ctgcggcccc gctccctcta cccggccgga cccggtctg cccccggccc caagccccac 120

caagcccccc gccctccgc cgcggtcca gccaggggcg cgccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225

Met Arg Pro Val Ala Leu Leu Leu Pro Ser Leu Ala Leu Leu

1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

20 25 30

cca gcc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro

35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu

50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly

65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro

85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn

100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala

115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser

130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser

145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro

165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly

180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile

195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr

210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr

225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp

245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe

260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln

275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly

290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly

305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser

325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala

340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val

355 360 365

act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329  
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala

370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
 Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
 385 390 395 400

acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425  
 Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
 405 410 415

ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473  
 Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
 420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
 Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
 435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
 Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
 450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
 Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
 465 470 475 480

gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ccg ccc cgc ccc 1665  
 Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro  
 485 490 495

cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713  
 Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
 500 505 510

tac gag act gga gag acg aga gaa tat gaa gtc tcc atc taggtggggg 1762  
 Tyr Glu Thr Gly Thr Arg Glu Tyr Glu Val Ser Ile  
 515 520 525

cagtctaggg aagtcaactc agacttcac cacagtccag cagcaaggct ccttgcttcc 1822

tgctgtcct ccacctctg tatataccac ctaggaggag atgccaccaa gccctcaaga 1882

agttgtgccc tccccgcct gcgatgccca ccatggccta tttcttgggt gtcattgccc 1942

acttggggcc ctgcattgg gccatgtaca gggggcatct acctgtgggg aagaacatag 2002

ctgggagcac aagcttaac agccagcatt ccttgagcct cctcatggc cctgggacca 2062

gcctggggaa cacanttagg caggagcagg gagttacctt gtttcacatg accaccaacc 2122

attcc 2127

<210> 20

<211> 525



<212> PRT

<213> Homo sapiens

<223> n 2077 can be A, G, C, or T.

<400> 20

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val  
355 360 365

Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro  
485 490 495

Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500 505 510

Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile  
515 520 525

<210> 21  
<211> 1988  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (178)..(1752)

<400> 21  
ccaggcgctg gccgtggtgc tgattctgtc aggcgctggc ggccgcagcg gcggtgacgg 60  
ctggcgcccc gctcctcta cccggccgga cccggctctg ccccgcgcc caagccccac 120  
caagcccccc gccctccgc cgcggtccca gcccagggcg cgcccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225  
Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

cca gcc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Ala Asn  
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561  
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val

355                      360                      365  
 act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329  
 Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
 370                      375                      380  
 act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
 Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
 385                      390                      395                      400  
 acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425  
 Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
 405                      410                      415  
 ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473  
 Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
 420                      425                      430  
 ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
 Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
 435                      440                      445  
 gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
 Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
 450                      455                      460  
 gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
 Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
 465                      470                      475                      480  
 gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ccg ccc cgc ccc 1665  
 Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro  
 485                      490                      495  
 cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713  
 Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
 500                      505                      510  
 tac gag act gga gag acg aga gaa tat gaa gtc tcc atc taggtggggg 1762  
 Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile  
 515                      520                      525  
 cagctaggg aagtaactc agactgcac cacagtccag cagcaaggct ccttgcttcc 1822  
 tgcgtccct ccacctctg tatataccac ctaggaggag atgccaccaa gccactttgt 1882  
 acatgtaatg tattatatgg ggtctgggct ccagccagag aacaatcttt tatttctgtt 1942  
 gtttccttat taaaatggtg tttttgaaa aaaaaaaaaa aaaaaa 1988

<210> 22  
 <211> 525

<212> PRT

<213> Homo sapiens

<400> 22

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe

260	265	270
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln		
275	280	285
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly		
290	295	300
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly		
305	310	315
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser		
325	330	335
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala		
340	345	350
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val		
355	360	365
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala		
370	375	380
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala		
385	390	395
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys		
405	410	415
Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly		
420	425	430
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu		
435	440	445
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu		
450	455	460
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu		
465	470	475
Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro		
485	490	495
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr		
500	505	510
Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile		
515	520	525

<211> 2143  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (178)..(1755)

<220>  
<223> n 2093 can be A, G, C, or T.

<400> 23  
ccaggcgctg gccgtggtgc tgattctgtc aggcgctggc gccggcagcg gcggtgacgg 60  
ctgcggcccc gctccctcta cccggccgga cccggtcttg cccccgcgcc caagccccac 120  
caagcccccc gccctccgcg cgcggtccca gcccaggcg cgcccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tgg ctg ctg gcg ctc ctg 225  
Met Arg Pro Val Ala Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561  
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140



gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val  
355 360 365

act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329  
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425  
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473  
Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

gcc cca cca gtg gga aaa agc tcc ctg cag ctg ccc cgc ccc cgc ccc 1665  
Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro  
485 490 495

cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713  
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500 505 510

tac gag act gga tct ctt tcc ttt gca gga gac gag aga ata 1755  
Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu Arg Ile  
515 520 525

tgaagtctcc atctaggtgg gggcagtcta gggaagtcaa ctcagacttg caccacagtc 1815

cagcagcaag gctcctgtct tctgtctgtc cctccacctc ctgtatatac cacctaggag 1875

gagatgccac caagccctca agaagttgtg cccttccccg cctgcgatgc ccacatggc 1935

ctattttctt ggtgtcattg cccacttggg gcccttgcac tgggcatgt acagggggca 1995

tctacctgtg gggaagaaca tagctgggag cacaagcttc aacagccagc attccttgag 2055

cctccttcat gccctgga ccagcctggg gaacacantt aggcaggagc agggagttac 2115

cttgttcac atgaccacca accattcc 2143

<210> 24

<211> 526

<212> PRT

<213> Homo sapiens

<223> n 2093 can be A, G, C, or T.

<400> 24

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr

210	215	220
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr		
225	230	235 240
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp		
245	250	255
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe		
260	265	270
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln		
275	280	285
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly		
290	295	300
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly		
305	310	315 320
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser		
325	330	335
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala		
340	345	350
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val		
355	360	365
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala		
370	375	380
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala		
385	390	395 400
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys		
405	410	415
Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly		
420	425	430
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu		
435	440	445
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu		
450	455	460
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu		
465	470	475 480
Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro		
485	490	495

Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500 505 510

Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu Arg Ile  
515 520 525

<210> 25  
<211> 1482  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (178)..(960)

<400> 25  
ccaggcgctg gccgtggtgc tgattctgtc aggcgctggc ggcggcagcg gcggtgacgg 60  
ctgcggcccc gctccctcta cccggccgga cccggctctg cccccgcgcc caagccccac 120  
caagcccccc gccctccgcg cgcggtccca gccagggcg cgccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225  
Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc acc atc atc acc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

cca ggt cag cta cct gct ggc ttg cag atg tgg aaa tgg gga tgg ggg 945  
Pro Gly Gln Leu Pro Ala Gly Leu Gln Met Trp Lys Trp Gly Trp Gly  
245 250 255

agg ctg cgg ggc ccc taaaagcctg tctctgacac tgtgccagcc tgcctgccc 1000  
Arg Leu Arg Gly Pro  
260

tttggcacca agggccagcc tgcaggaggc atgtagattg gacccagata gacctgagct 1060

caaatcctga ttcttcagcc aagtacagtg gctcatgcct gtaatccag cactttggga 1120

ggcagaggcc agtggatcat ctgaggtcag gaggltcaaga cctcctggc caacatggcg 1180

aaacaccatc tctactaaaa atacaaaaat gagccgggca tgggtgtggg cacctgtaat 1240

cccagctact cgggaggctg aggcaggaga atcactcaaa cctgggaggc agagggttga 1300

gtgagctgag attgcacat tgcactccag cctgggcaac agagcgagac tctgtctcaa 1360

aaaagaaaa atcttgattc ttccaactat aacatgaccc taggaattct atttaacatc 1420

tcattcttga gcctcatctg taaaatggca ataagaaaat aaacttctgg ctagaataaaa 1480

aa

1482

<210> 26

<211> 261

<212> PRT

<213> Homo sapiens

<400> 26

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu

1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro

35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu

50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly

65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro

85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn

100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala

115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser

130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser

145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro

165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly

180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile

195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr

210 215 220

Thr Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

Pro Gly Gln Leu Pro Ala Gly Leu Gln Met Trp Lys Trp Gly Trp Gly  
245 250 255

Arg Leu Arg Gly Pro  
260

<210> 27  
<211> 3336  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (120)..(2639)

<220>  
<223> n 3325 can be A, G, C, or T.

<400> 27  
cgccggtggc tcggcggcgg cgccggcggc ggccggcggc gcggcggcgg cgtcgtctac 60

ctccagctcc tctccctcc tctccgtct cctcctctct ctctccatct gctgtggtt 119

atg gcc tgt cgc tgg agc aca aaa gag tct ccg cgg tgg agg tct gcg 167  
Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg Trp Arg Ser Ala  
1 5 10 15

ttg ctc ttg ctt ttc ctc gct ggg gtg tac gct tgt gga gag act cca 215  
Leu Leu Leu Leu Phe Leu Ala Gly Val Tyr Ala Cys Gly Glu Thr Pro  
20 25 30

gag caa ata cga gca cca agt ggc ata atc aca agc cca ggc tgg cct 263  
Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro Gly Trp Pro  
35 40 45

tct gaa tat cct gca aaa atc aac tgt agc tgg ttc ata agg gca aac 311  
Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile Arg Ala Asn  
50 55 60

cca ggc gaa atc att act ata agt ttt cag gat ttt gat att caa gga 359  
Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp Ile Gln Gly  
65 70 75 80

tcc aga agg tgc aat ttg gac tgg ttg aca ata gaa aca tac aag aat 407  
Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr Tyr Lys Asn  
85 90 95

att gaa agt tac aga gct tgt ggt tcc aca att cca cct ccg tat atc 455



Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro Pro Tyr Ile  
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tct tca caa gac cac atc tgg att agg ttt cat tcg gat gac aac atc 503  
 Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp Asp Asn Ile  
 115 120 125

tct aga aag ggt ttc aga ctg gca tat ttt tca ggg aaa tct gag gaa 551  
 Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys Ser Glu Glu  
 130 135 140

cca aat tgt gct tgt gat cag ttt cgt tgt ggt aat gga aag tgt ata 599  
 Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly Lys Cys Ile  
 145 150 155 160

cca gaa gcc tgg aaa tgc aat aac atg gat gaa tgt gga gat agt tcc 647  
 Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly Asp Ser Ser  
 165 170 175

gat gaa gag atc tgt gcc aaa gaa gca aat cct cca act gct gct gct 695  
 Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr Ala Ala Ala  
 180 185 190

ttt caa ccc tgt gct tac aac cag ttc cag tgt tta tcc cgt ttt acc 743  
 Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser Arg Phe Thr  
 195 200 205

aaa gtt tac act tgc ctc ccc gaa tct tta aaa tgt gat ggg aac att 791  
 Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp Gly Asn Ile  
 210 215 220

gac tgc ctt gac cta gga gat gag ata gac tgt gat gtg cca aca tgt 839  
 Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val Pro Thr Cys  
 225 230 235 240

ggg caa tgg cta aaa tat ttt tat ggt act ttt aat tct ccc aat tat 887  
 Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser Pro Asn Tyr  
 245 250 255

cca gac ttt tat cct cct gga agc aat tgc acc tgg tta ata gac act 935  
 Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu Ile Asp Thr  
 260 265 270

ggt gat cac cgt aaa gtc att tta cgc ttc act gac ttt aaa ctt gat 983  
 Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe Lys Leu Asp  
 275 280 285

ggt act ggt tat ggt gat tat gtc aaa ata tat gat gga tta gag gag 1031  
 Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly Leu Glu Glu  
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aat cca cac aag ctt ttg cgt gtg ttg aca gct ttt gat tct cat gca 1079  
 Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp Ser His Ala

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 Trp Val Cys Asp Ser Gln Asp Asp Cys Gly Asp Gly Ser Asp Glu Glu  
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 Asn Cys Pro Val Ile Val Pro Thr Arg Val Ile Thr Ala Ala Val Ile  
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 ggg agc ctc atc tgt ggc ctg tta ctc gtc ata gca ttg gga tgt act 1607  
 Gly Ser Leu Ile Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr  
                   485                    490                    495  
 tgt aag ctt tat tct ctg aga atg ttt gaa aga aga tca ttt gaa aca 1655  
 Cys Lys Leu Tyr Ser Leu Arg Met Phe Glu Arg Arg Ser Phe Glu Thr  
                   500                    505                    510  
 cag ttg tca aga gtg gaa gca gaa ttg tta aga aga gaa gct cct ccc 1703  
 Gln Leu Ser Arg Val Glu Ala Glu Leu Leu Arg Arg Glu Ala Pro Pro  
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tcg tat gga caa ttg att gct cag ggt tta att cca cca gtt gaa gat 1751  
Ser Tyr Gly Gln Leu Ile Ala Gln Gly Leu Ile Pro Pro Val Glu Asp  
530 535 540

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Phe Pro Val Cys Ser Pro Asn Gln Ala Ser Val Leu Glu Asn Leu Arg  
545 550 555 560

cta gcg gta cga tct cag ctt gga ttt act tca gtc agg ctt cct atg 1847  
Leu Ala Val Arg Ser Gln Leu Gly Phe Thr Ser Val Arg Leu Pro Met  
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gca ggc aga tca agc aac att tgg aac cgt att ttt aat ttt gca aga 1895  
Ala Gly Arg Ser Ser Asn Ile Trp Asn Arg Ile Phe Asn Phe Ala Arg  
580 585 590

tca cgt cat tct ggg tca ttg gct ttg gtc tca gca gat gga gat gag 1943  
Ser Arg His Ser Gly Ser Leu Ala Leu Val Ser Ala Asp Gly Asp Glu  
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gtt gtc cct agt cag agt acc agt aga gaa cct gag aga aat cat act 1991  
Val Val Pro Ser Gln Ser Thr Ser Arg Glu Pro Glu Arg Asn His Thr  
610 615 620

cac aga agt ttg ttt tcc gtg gag tct gat gat aca gac aca gaa aat 2039  
His Arg Ser Leu Phe Ser Val Glu Ser Asp Asp Thr Asp Thr Glu Asn  
625 630 635 640

gag aga aga gat atg gca gga gca tct ggt ggg gtt gca gct cct ttg 2087  
Glu Arg Arg Asp Met Ala Gly Ala Ser Gly Val Ala Ala Pro Leu  
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cct caa aaa gtc cct ccc aca acg gca gta gaa gcg aca gta gga gca 2135  
Pro Gln Lys Val Pro Pro Thr Thr Ala Val Glu Ala Thr Val Gly Ala  
660 665 670

tgt gca agt tcc tca act cag agt acc cga ggt ggt cat gca gat aat 2183  
Cys Ala Ser Ser Ser Thr Gln Ser Thr Arg Gly Gly His Ala Asp Asn  
675 680 685

gga agg gat gtg aca agt gtg gaa ccc cca agt gtg agt cca gca cgt 2231  
Gly Arg Asp Val Thr Ser Val Glu Pro Pro Ser Val Ser Pro Ala Arg  
690 695 700

cac cag ctt aca agt gca ctc agt cgt atg act cag ggg cta cgc tgg 2279  
His Gln Leu Thr Ser Ala Leu Ser Arg Met Thr Gln Gly Leu Arg Trp  
705 710 715 720

gta cgt ttt aca tta gga cga tca agt tcc cta agt cag aac cag agt 2327  
Val Arg Phe Thr Leu Gly Arg Ser Ser Ser Leu Ser Gln Asn Gln Ser  
725 730 735

cct ttg aga caa ctt gat aat ggg gta agt gga aga gaa gat gat gat 2375  
Pro Leu Arg Gln Leu Asp Asn Gly Val Ser Gly Arg Glu Asp Asp Asp  
740 745 750

gat gtt gaa atg cta att cca att tct gat gga tct tca gac ttt gat 2423  
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755 760 765

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Val Asn Asp Cys Ser Arg Pro Leu Leu Asp Leu Ala Ser Asp Gln Gly  
770 775 780

caa ggg ctt aga caa cca tat aat gca aca aat cct gga gta agg cca 2519  
Gln Gly Leu Arg Gln Pro Tyr Asn Ala Thr Asn Pro Gly Val Arg Pro  
785 790 795 800

agt aat cga gat ggc ccc tgt gag cgc tgt ggt att gtc cac act gcc 2567  
Ser Asn Arg Asp Gly Pro Cys Glu Arg Cys Gly Ile Val His Thr Ala  
805 810 815

cag ata cca gac act tgc tta gaa gta aca ctg aaa aac gaa acg agt 2615  
Gln Ile Pro Asp Thr Cys Leu Glu Val Thr Leu Lys Asn Glu Thr Ser  
820 825 830

gat gat gag gct ttg tta ctt tgt taggtacgaa tcacataagg gagattgtat 2669  
Asp Asp Glu Ala Leu Leu Cys  
835 840

acaagttgga gcaatatcca ttattattt tgtaacttta cagltaaact agttttagtt 2729

taaaaagaaa aaatgcaggg tgatttctta ttattatag ttacgtgca tgggttaaatt 2789

cgacaacttg taactctatg aacttagagt ttactatttt agcagctaaa aatgcatcac 2849

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ctgtagtcca ctgtagaaat gtggctgctg aaactcattt gattgtcatt ttatctatc 2969

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atcattatca tatgaacttg tcagtgggaa acaaactgtc taaaaattta tctcttacgt 3209

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35 40 45  
Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile Arg Ala Asn  
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Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp Ile Gln Gly  
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Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr Tyr Lys Asn  
85 90 95  
Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro Pro Tyr Ile  
100 105 110  
Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp Asp Asn Ile  
115 120 125  
Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys Ser Glu Glu  
130 135 140  
Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly Lys Cys Ile  
145 150 155 160  
Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly Asp Ser Ser  
165 170 175  
Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr Ala Ala Ala  
180 185 190  
Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser Arg Phe Thr  
195 200 205  
Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp Gly Asn Ile  
210 215 220  
Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val Pro Thr Cys  
225 230 235 240  
Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser Pro Asn Tyr

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Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe Lys Leu Asp		
275	280	285
Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly Leu Glu Glu		
290	295	300
Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp Ser His Ala		
305	310	315
Pro Leu Thr Val Val Ser Ser Ser Gly Gln Ile Arg Val His Phe Cys		
325	330	335
Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr Tyr Gln Val		
340	345	350
Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly Asn Trp Gly		
355	360	365
Cys Tyr Thr Glu Gln Gln Arg Cys Asp Gly Tyr Trp His Cys Pro Asn		
370	375	380
Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu Glu Phe Pro		
385	390	395
Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg Cys Asn Tyr		
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Gln Asn His Cys Pro Asn Gly Ser Asp Glu Lys Asn Cys Phe Phe Cys		
420	425	430
Gln Pro Gly Asn Phe His Cys Lys Asn Asn Arg Cys Val Phe Glu Ser		
435	440	445
Trp Val Cys Asp Ser Gln Asp Asp Cys Gly Asp Gly Ser Asp Glu Glu		
450	455	460
Asn Cys Pro Val Ile Val Pro Thr Arg Val Ile Thr Ala Ala Val Ile		
465	470	475
Gly Ser Leu Ile Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr		
485	490	495
Cys Lys Leu Tyr Ser Leu Arg Met Phe Glu Arg Arg Ser Phe Glu Thr		
500	505	510
Gln Leu Ser Arg Val Glu Ala Glu Leu Leu Arg Arg Glu Ala Pro Pro		
515	520	525

Ser Tyr Gly Gln Leu Ile Ala Gln Gly Leu Ile Pro Pro Val Glu Asp  
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Phe Pro Val Cys Ser Pro Asn Gln Ala Ser Val Leu Glu Asn Leu Arg  
 545 550 555 560

Leu Ala Val Arg Ser Gln Leu Gly Phe Thr Ser Val Arg Leu Pro Met  
 565 570 575

Ala Gly Arg Ser Ser Asn Ile Trp Asn Arg Ile Phe Asn Phe Ala Arg  
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Ser Arg His Ser Gly Ser Leu Ala Leu Val Ser Ala Asp Gly Asp Glu  
 595 600 605

Val Val Pro Ser Gln Ser Thr Ser Arg Glu Pro Glu Arg Asn His Thr  
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His Arg Ser Leu Phe Ser Val Glu Ser Asp Asp Thr Asp Thr Glu Asn  
 625 630 635 640

Glu Arg Arg Asp Met Ala Gly Ala Ser Gly Gly Val Ala Ala Pro Leu  
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Pro Gln Lys Val Pro Pro Thr Thr Ala Val Glu Ala Thr Val Gly Ala  
 660 665 670

Cys Ala Ser Ser Ser Thr Gln Ser Thr Arg Gly Gly His Ala Asp Asn  
 675 680 685

Gly Arg Asp Val Thr Ser Val Glu Pro Pro Ser Val Ser Pro Ala Arg  
 690 695 700

His Gln Leu Thr Ser Ala Leu Ser Arg Met Thr Gln Gly Leu Arg Trp  
 705 710 715 720

Val Arg Phe Thr Leu Gly Arg Ser Ser Ser Leu Ser Gln Asn Gln Ser  
 725 730 735

Pro Leu Arg Gln Leu Asp Asn Gly Val Ser Gly Arg Glu Asp Asp Asp  
 740 745 750

Asp Val Glu Met Leu Ile Pro Ile Ser Asp Gly Ser Ser Asp Phe Asp  
 755 760 765

Val Asn Asp Cys Ser Arg Pro Leu Leu Asp Leu Ala Ser Asp Gln Gly  
 770 775 780

Gln Gly Leu Arg Gln Pro Tyr Asn Ala Thr Asn Pro Gly Val Arg Pro  
 785 790 795 800

Ser Asn Arg Asp Gly Pro Cys Glu Arg Cys Gly Ile Val His Thr Ala  
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Gln Ile Pro Asp Thr Cys Leu Glu Val Thr Leu Lys Asn Glu Thr Ser  
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atg gcc tgt cgc tgg agc aca aaa gag tct ccg cgg tgg agg tct gcg 167  
Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg Trp Arg Ser Ala  
1 5 10 15

ttg ctc ttg ctt ttc ctc gct ggg gtg tac gga aat ggt gct ctt gca 215  
Leu Leu Leu Leu Phe Leu Ala Gly Val Tyr Gly Asn Gly Ala Leu Ala  
20 25 30

gaa cat tct gaa aat gtg cat att tca gga gtg tca act gct tgt gga 263  
Glu His Ser Glu Asn Val His Ile Ser Gly Val Ser Thr Ala Cys Gly  
35 40 45

gag act cca gag caa ata cga gca cca agt ggc ata atc aca agc cca 311  
Glu Thr Pro Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro  
50 55 60

ggc tgg cct tct gaa tat cct gca aaa atc aac tgt agc tgg ttc ata 359  
Gly Trp Pro Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile  
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agg gca aac cca ggc gaa atc att act ata agt ttt cag gat ttt gat 407  
Arg Ala Asn Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp  
85 90 95

att caa gga tcc aga agg tgc aat ttg gac tgg ttg aca ata gaa aca 455  
Ile Gln Gly Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr  
100 105 110

tac aag aat att gaa agt tac aga gct tgt ggt tcc aca att cca cct 503  
Tyr Lys Asn Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro



115

120

125

ccg tat atc tct tca caa gac cac atc tgg att agg ttt cat tcg gat 551  
Pro Tyr Ile Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp  
130 135 140

gac aac atc tct aga aag ggt ttc aga ctg gca tat ttt tca ggg aaa 599  
Asp Asn Ile Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys  
145 150 155 160

tct gag gaa cca aat tgt gct tgt gat cag ttt cgt tgt ggt aat gga 647  
Ser Glu Glu Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly  
165 170 175

aag tgt ata cca gaa gcc tgg aaa tgt aat aac atg gat gaa tgt gga 695  
Lys Cys Ile Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly  
180 185 190

gat agt tcc gat gaa gag atc tgt gcc aaa gaa gca aat cct cca act 743  
Asp Ser Ser Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr  
195 200 205

gct gct gct ttt caa ccc tgt gct tac aac cag ttc cag tgt tta tcc 791  
Ala Ala Ala Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser  
210 215 220

cgt ttt acc aaa gtt tac act tgc ctc ccc gaa tct tta aaa tgt gat 839  
Arg Phe Thr Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp  
225 230 235 240

ggg aac att gac tgc ctt gac cta gga gat gag ata gac tgt gat gtg 887  
Gly Asn Ile Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val  
245 250 255

cca aca tgt ggg caa tgg cta aaa tat ttt tat ggt act ttt aat tct 935  
Pro Thr Cys Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser  
260 265 270

ccc aat tat cca gac ttt tat cct cct gga agc aat tgc acc tgg tta 983  
Pro Asn Tyr Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu  
275 280 285

ata gac act ggt gat cac cgt aaa gtc att tta cgc ttc act gac ttt 1031  
Ile Asp Thr Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe  
290 295 300

aaa ctt gat ggt act ggt tat ggt gat tat gtc aaa ata tat gat gga 1079  
Lys Leu Asp Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly  
305 310 315 320

tta gag gag aat cca cac aag ctt ttg cgt gtg ttg aca gct ttt gat 1127  
Leu Glu Glu Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp  
325 330 335

tct cat gca cct ctt aca gtt gtt tct tct tct gga cag ata agg gta 1175  
Ser His Ala Pro Leu Thr Val Val Ser Ser Ser Gly Gln Ile Arg Val  
340 345 350

cat ttt tgt gct gat aaa gtg aat gct gca agg gga ttt aat gct act 1223  
His Phe Cys Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr  
355 360 365

tac caa gta gat ggg ttc tgt ttg cca tgg gaa ata ccc tgt gga ggt 1271  
Tyr Gln Val Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly  
370 375 380

aac tgg ggg tgt tat act gag cag cag cgt cgt gat ggg tat tgg cat 1319  
Asn Trp Gly Cys Tyr Thr Glu Gln Gln Arg Arg Asp Gly Tyr Trp His  
385 390 395 400

tgc cca aat gga agg gat gaa acc aat tgt acc atg tgc cag aag gaa 1367  
Cys Pro Asn Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu  
405 410 415

gaa ttt cca tgt tcc cga aat ggt gtc tgt tat cct cgt tct gat cgc 1415  
Glu Phe Pro Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg  
420 425 430

tgc aac tac cag aat cat tgc cca aat ggc aaa cag aac cca tct act 1463  
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35 40 45

Glu Thr Pro Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro  
50 55 60

Gly Trp Pro Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile  
65 70 75 80

Arg Ala Asn Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp  
 85 90 95  
 Ile Gln Gly Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr  
 100 105 110  
 Tyr Lys Asn Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro  
 115 120 125  
 Pro Tyr Ile Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp  
 130 135 140  
 Asp Asn Ile Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys  
 145 150 155 160  
 Ser Glu Glu Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly  
 165 170 175  
 Lys Cys Ile Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly  
 180 185 190  
 Asp Ser Ser Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr  
 195 200 205  
 Ala Ala Ala Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser  
 210 215 220  
 Arg Phe Thr Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp  
 225 230 235 240  
 Gly Asn Ile Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val  
 245 250 255  
 Pro Thr Cys Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser  
 260 265 270  
 Pro Asn Tyr Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu  
 275 280 285  
 Ile Asp Thr Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe  
 290 295 300  
 Lys Leu Asp Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly  
 305 310 315 320  
 Leu Glu Glu Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp  
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 Ser His Ala Pro Leu Thr Val Val Ser Ser Ser Gly Gln Ile Arg Val  
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 His Phe Cys Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr

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 Cys Pro Asn Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu  
                     405                      410                      415  
 Glu Phe Pro Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg  
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Trp

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 ctccgggagc ggcagcagta gcccgggcgg cgagggtgg gggttcctcg agactctcag 120  
 aggggcgcct cccatcggcg cccaccaccc caactgttc ctgcgcgcc actgcgctgc 180

gccccaggac ccgctgcccc ac atg gat ttt ctc ctg gcg ctg gtg ctg gta 232  
                     Met Asp Phe Leu Leu Ala Leu Val Leu Val  
                     1                      5                      10

tcc tcg ctc tac ctg cag gcg gcc gcc gag tac gac ggg agg tgg ccc 280  
 Ser Ser Leu Tyr Leu Gln Ala Ala Ala Glu Tyr Asp Gly Arg Trp Pro  
                     15                      20                      25

agg caa ata gtg tca tcg att ggc cta tgt cgt tat ggt ggg agg att 328  
 Arg Gln Ile Val Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile  
                     30                      35                      40

gac tgc tgc tgg ggc tgg gct cgc cag tct tgg gga cag tgt cag cct 376  
 Asp Cys Cys Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro  
                     45                      50                      55

ttc tac gtc tta agg cag aga ata gcc agg ata agg tgc cag ctc aaa 424  
Phe Tyr Val Leu Arg Gln Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys  
60 65 70

gct gtg tgc caa cca cga tgc aaa cat ggt gaa tgt atc ggg cca aac 472  
Ala Val Cys Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn  
75 80 85 90

aag tgc aag tgt cat cct ggt tat gct gga aaa acc tgt aat caa gcc 520  
Lys Cys Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Ala  
95 100 105

gta ggt ttt gaa aga tgt atg gtt cca gcc ggg cgc cgt ggc tct acc 568  
Val Gly Phe Glu Arg Cys Met Val Pro Ala Gly Arg Arg Gly Ser Thr  
110 115 120

ctg taatcccagc actttggaag gccgaggcgg gcggtcacg aggtcaggat 621  
Leu

atcgagacca tcctggctaa cacggtgaaa ccccatctct actaaaaata caaaaaaaaa 681

aaaaaaaaa 691

<210> 32  
<211> 123  
<212> PRT  
<213> Homo sapiens

<400> 32  
Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu Gln  
1 5 10 15

Ala Ala Ala Glu Tyr Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser  
20 25 30

Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp  
35 40 45

Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Phe Tyr Val Leu Arg Gln  
50 55 60

Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys Ala Val Cys Gln Pro Arg  
65 70 75 80

Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro  
85 90 95

Gly Tyr Ala Gly Lys Thr Cys Asn Gln Ala Val Gly Phe Glu Arg Cys  
100 105 110

Met Val Pro Ala Gly Arg Arg Gly Ser Thr Leu

115

120

<210> 33  
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 <213> Homo sapiens

<220>  
 <221> CDS  
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<400> 33  
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 ctccgggagc ggcagcagta gcccgggagg cgagggtgg gggttctcg agactctcag 120  
 aggggagcct cccatcgagg cccaccaccc caacctgtc ctgcgcgcc actgcgctgc 180  
 gcccaggagc ccgctgccc ac atg gat ttt ctc ctg gcg ctg gtg ctg gta 232  
 Met Asp Phe Leu Leu Ala Leu Val Leu Val  
 1 5 10

tcc tgg ctc tac ctg cag gcg gcc gcc gag ttc gac ggg agg tgg ccc 280  
 Ser Ser Leu Tyr Leu Gln Ala Ala Glu Phe Asp Gly Arg Trp Pro  
 15 20 25

agg caa ata gtg tca tgg att ggc cta tgt cgt tat ggt ggg agg att 328  
 Arg Gln Ile Val Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile  
 30 35 40

gac tgc tgc tgg ggc tgg gct cgc cag tct tgg gga cag tgt cag cct 376  
 Asp Cys Cys Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro  
 45 50 55

ttc tac gtc tta agg cag aga ata gcc agg ata agg tgc cag ctc aaa 424  
 Phe Tyr Val Leu Arg Gln Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys  
 60 65 70

gct gtg tgc caa cca cga tgc aaa cat ggt gaa tgt atc ggg cca aac 472  
 Ala Val Cys Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn  
 75 80 85 90

aag tgc aag tgt cat cct ggt tat gct gga aaa acc tgt att caa gtt 520  
 Lys Cys Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Ile Gln Val  
 95 100 105

tta aat gag tgt ggc ctg aag ccc cgg ccc tgt aag cac agg tgc atg 568  
 Leu Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met  
 110 115 120

aac act tac ggc agc tac aag tgc tac tgt ctc aac gga tat atg ctc 616

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met Leu  
125 130 135

atg ccg gat ggt tcc tgc tca agt gcc ctg acc tgc tcc atg gca aac 664  
Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met Ala Asn  
140 145 150

tgt cag tat ggc tgt gat gtt gtt aaa gga caa ata cgg tgc cag tgc 712  
Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg Cys Gln Cys  
155 160 165 170

cca tcc cct ggc ctg cag ctg gct cct gat ggg agg acc tgt gta gat 760  
Pro Ser Pro Gly Leu Gln Leu Ala Pro Asp Gly Arg Thr Cys Val Asp  
175 180 185

gtt gat gaa tgt gct aca gga aga gcc tcc tgc cct aga ttt agg caa 808  
Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys Pro Arg Phe Arg Gln  
190 195 200

tgt gtc aac act ttt ggg agc tac atc tgc aag tgt cat aaa ggc ttc 856  
Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys Lys Cys His Lys Gly Phe  
205 210 215

gat ctc atg tat att gga ggc aaa tat caa tgt cat gac ata gac gaa 904  
Asp Leu Met Tyr Ile Gly Gly Lys Tyr Gln Cys His Asp Ile Asp Glu  
220 225 230

tgc tca ctt ggt cag tat cag tgc agc agc ttt gct cga tgt tat aac 952  
Cys Ser Leu Gly Gln Tyr Gln Cys Ser Ser Phe Ala Arg Cys Tyr Asn  
235 240 245 250

gta cgt ggg tcc tac aag tgc aaa tgt aaa gaa gga tac cag ggt gat 1000  
Val Arg Gly Ser Tyr Lys Cys Lys Cys Lys Glu Gly Tyr Gln Gly Asp  
255 260 265

gga ctg act tgt gtg tat atc cca aaa gtt atg att gaa cct tca ggt 1048  
Gly Leu Thr Cys Val Tyr Ile Pro Lys Val Met Ile Glu Pro Ser Gly  
270 275 280

cca att cat gta cca aag gga aat ggt acc att tta aag ggt gac aca 1096  
Pro Ile His Val Pro Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr  
285 290 295

gga aat aat aat tgg att cct gat gtt gga agt act tgg tgg cct ccg 1144  
Gly Asn Asn Asn Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro  
300 305 310

aag aca cca tat att cct cct atc att acc aac agg cct act tct aag 1192  
Lys Thr Pro Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys  
315 320 325 330

cca aca aca aga cct aca cca aag cca aca cca att cct act cca cca 1240  
Pro Thr Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro

335	340	345	
cca cca cca ccc ctg cca aca gag ctc aga aca cct cta cca cct aca 1288			
Pro Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr			
350	355	360	
acc cca gaa agg cca acc acc gga ctg aca act ata gca cca gct gcc 1336			
Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala Ala			
365	370	375	
agt aca cct cca gga ggg att aca gtt gac aac agg gta cag aca gac 1384			
Ser Thr Pro Pro Gly Ile Thr Val Asp Asn Arg Val Gln Thr Asp			
380	385	390	
cct cag aaa ccc aga gga gat gtg ttc att cca cgg caa cct tca aat 1432			
Pro Gln Lys Pro Arg Gly Asp Val Phe Ile Pro Arg Gln Pro Ser Asn			
395	400	405	410
gac ttg ttt gaa ata ttt gaa ata gaa aga gga gtc agt gca gac gat 1480			
Asp Leu Phe Glu Ile Phe Glu Ile Glu Arg Gly Val Ser Ala Asp Asp			
415	420	425	
gaa gca aag gat gat cca ggt gtt ctg gta cac agt tgt aat ttt gac 1528			
Glu Ala Lys Asp Asp Pro Gly Val Leu Val His Ser Cys Asn Phe Asp			
430	435	440	
cat gga ctt tgt gga tgg atc agg gag aaa gac aat gac ttg cac tgg 1576			
His Gly Leu Cys Gly Trp Ile Arg Glu Lys Asp Asn Asp Leu His Trp			
445	450	455	
gaa cca atc agg gac cca gca ggt gga caa tat ctg aca gtg tgg gca 1624			
Glu Pro Ile Arg Asp Pro Ala Gly Gly Gln Tyr Leu Thr Val Ser Ala			
460	465	470	
gcc aaa gcc cca ggg gga aaa gct gca cgc ttg gtg cta cct ctc ggc 1672			
Ala Lys Ala Pro Gly Gly Lys Ala Ala Arg Leu Val Leu Pro Leu Gly			
475	480	485	490
cgc ctt atg cat tca ggg gac ctg tgc ctg tca ttc agg cac aag gtg 1720			
Arg Leu Met His Ser Gly Asp Leu Cys Leu Ser Phe Arg His Lys Val			
495	500	505	
acg ggg ctg cac tct ggc aca ctc cag gtg ttt gtg aga aaa cac ggt 1768			
Thr Gly Leu His Ser Gly Thr Leu Gln Val Phe Val Arg Lys His Gly			
510	515	520	
gcc cac gga gca gcc ctg tgg gga aga aat ggt ggc cat ggc tgg agg 1816			
Ala His Gly Ala Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg			
525	530	535	
caa aca cag atc acc ttg cga ggg gct gac atc aag agc gtc gtc ttc 1864			
Gln Thr Gln Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Val Val Phe			
540	545	550	



aaa ggt gaa aaa agg cgt ggt cac act ggg gag att gga tta gat gat 1912

Lys Gly Glu Lys Arg Arg Gly His Thr Gly Glu Ile Gly Leu Asp Asp

555 560 565 570

gtg agc ttg aaa aaa ggc cac tgc tct gaa gaa cgc taacaactcc 1958

Val Ser Leu Lys Lys Gly His Cys Ser Glu Glu Arg

575 580

agaactaaca atgaactcct atgtgctct atcctctttt tccaattctc atcttctctc 2018

ctcttctccc tttatcagg cctaggagaa gagtgggtca gtgggtcaga aggaagtcta 2078

tttggtgacc caggttcttc tggcctgctt ttgt 2112

<210> 34

<211> 582

<212> PRT

<213> Homo sapiens

<400> 34

Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu Gln

1 5 10 15

Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser

20 25 30

Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp

35 40 45

Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Phe Tyr Val Leu Arg Gln

50 55 60

Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys Ala Val Cys Gln Pro Arg

65 70 75 80

Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro

85 90 95

Gly Tyr Ala Gly Lys Thr Cys Ile Gln Val Leu Asn Glu Cys Gly Leu

100 105 110

Lys Pro Arg Pro Cys Lys His Arg Cys Met Asn Thr Tyr Gly Ser Tyr

115 120 125

Lys Cys Tyr Cys Leu Asn Gly Tyr Met Leu Met Pro Asp Gly Ser Cys

130 135 140

Ser Ser Ala Leu Thr Cys Ser Met Ala Asn Cys Gln Tyr Gly Cys Asp

145 150 155 160

Val Val Lys Gly Gln Ile Arg Cys Gln Cys Pro Ser Pro Gly Leu Gln

165	170	175
Leu Ala Pro Asp Gly Arg Thr Cys Val Asp Val Asp Glu Cys Ala Thr		
180	185	190
Gly Arg Ala Ser Cys Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly		
195	200	205
Ser Tyr Ile Cys Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly		
210	215	220
Gly Lys Tyr Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr		
225	230	235
Gln Cys Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys		
245	250	255
Cys Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr		
260	265	270
Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro Lys		
275	280	285
Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn Trp Ile		
290	295	300
Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro Tyr Ile Pro		
305	310	315
Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr Thr Arg Pro Thr		
325	330	335
Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro Pro Pro Leu Pro		
340	345	350
Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr Thr Pro Glu Arg Pro Thr		
355	360	365
Thr Gly Leu Thr Thr Ile Ala Pro Ala Ala Ser Thr Pro Pro Gly Gly		
370	375	380
Ile Thr Val Asp Asn Arg Val Gln Thr Asp Pro Gln Lys Pro Arg Gly		
385	390	395
Asp Val Phe Ile Pro Arg Gln Pro Ser Asn Asp Leu Phe Glu Ile Phe		
405	410	415
Glu Ile Glu Arg Gly Val Ser Ala Asp Asp Glu Ala Lys Asp Asp Pro		
420	425	430
Gly Val Leu Val His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp		
435	440	445

Ile Arg Glu Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro  
450 455 460

Ala Gly Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly  
465 470 475 480

Lys Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly  
485 490 495

Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser Gly  
500 505 510

Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala Ala Leu  
515 520 525

Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln Ile Thr Leu  
530 535 540

Arg Gly Ala Asp Ile Lys Ser Val Val Phe Lys Gly Glu Lys Arg Arg  
545 550 555 560

Gly His Thr Gly Glu Ile Gly Leu Asp Asp Val Ser Leu Lys Lys Gly  
565 570 575

His Cys Ser Glu Glu Arg  
580

<210> 35

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 35

gaattcttgc caagagagta cacagtcatt aatg

34

<210> 36

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 36

aagcttttgc caagagagta cacagtcatt aatg

34

<210> 37  
<211> 30  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 37  
ctcgagtttc atattcttt caatccagtc 30

<210> 38  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 38  
tgtggccagg ttctgcga 18

<210> 39  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 39  
cttgacaagg ctggatct 18

<210> 40  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 40  
cctaccaaga agccagcc 18

<210> 41  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 41  
tcgcagaacc tggccaca 18

<210> 42  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 42  
agatccagcc ttgtcaag 18

<210> 43  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 43  
ggctggcttc ttggtagg 18

<210> 44  
<211> 21  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 44  
caggcagcca tctacaggag g 21

<210> 45  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 45  
cctcctgtag atggctgcct g 21

<210> 46  
<211> 18  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 46  
caggagtccc acatcact 18

<210> 47  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 47  
agtgatgtgg gactcctg 18

<210> 48  
<211> 38  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 48  
gctagccacc atggagctgg gttgctggac gcagttgg 38

<210> 49  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 49  
aggacgtgga gtgaggatcc tatgctctgg atagg 35

<210> 50  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 50

ctcgtcctcg agggtaagcc tatccctaac

30

<210> 51

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 51

ctcgtcgggc cctgatcag cgggtttaa c

31

<210> 52

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 52

ggatccaaat cctgtccatc tgtgtgtcgc tg

32

<210> 53

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 53

ctcgagagcc aaaggtaa tggggtttt gtaag

35

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 54  
cgagacagca actatctc 18

<210> 55  
<211> 18  
<212> DNA  
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<220>  
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<400> 55  
cgactggata tgtccaat 18

<210> 56  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 56  
acaattactg tgaagtct 18

<210> 57  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 57  
gagatagttg ctgtctcg 18

<210> 58  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 58  
attggacata tccagtcg 18

<210> 59



<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 59  
agacttcaca gtaattgt 18

<210> 60  
<211> 34  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 60  
ggatccgagg ctgaaggcaa tgcaagctgc acag 34

<210> 61  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 61  
tcgagcagtg gaatgtaggt gctgtgaatg cag 33

<210> 62  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 62  
ggatccgcgg tcctgtggaa gcatgtgcgg ctg 33

<210> 63  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 63

ctcgagcgtg ttgcacacca gcacatctgc

30

<210> 64

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 64

gacgtggccc tcatcgcaa c

21

<210> 65

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 65

ctaggcgagg agtacattct g

21

<210> 66

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 66

ctggaccggg ctgagcaa

18

<210> 67

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 67

gttgccgatg agggccacgt c

21

<210> 68  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 68  
cagaatgtac tcctgccta g 21

<210> 69  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 69  
ttgctcagcc cggtccag 18

<210> 70  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 70  
ggtacctgtg gagagactcc agagcaaata cga 33

<210> 71  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 71  
ctcgagagtg atgactcttg taggcacgat tac 33

<210> 72  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 72  
gcttgatc agttcgt 18

<210> 73  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 73  
tgcacctgt taatagac 18

<210> 74  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 74  
actgagcagc agcgtgt 18

<210> 75  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 75  
acgaaactga tcacaagc 18

<210> 76  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 76

tattaaccag gtgcaatt 18

<210> 77  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 77  
acaacgctgc tgctcagt 18

<210> 78  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 78  
ggatccgagt acgacgggag gtggcccagg 30

<210> 79  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 79  
ctcgagcagg gtagagccac ggcgcccggc tggaac 36

<210> 80  
<211> 261  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: AMPLIFICATION  
PRODUCT 16467945.0.85-S259.A

<400> 80  
gagtagcagc ggaggtggcc caggcaaata gtgtcatcga ttggcctatg tcgttatggt 60  
gggaggattg actgctgctg gggctgggct cgccagtctt ggggacagtg tcagcctgtg 120  
tgccaaccac gatgcaaaca tggatgaatgt atcgggcca acaagtgcaa gtgtcatcct 180  
ggttatgctg gaaaaacctg taatcaagcc gtaggttttg aaagatgtat ggttcagcc 240

gggcgccgtg gctctaccct g

261

<210> 81

<211> 1638

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CONSTRUCT

16467945.0.88-S261.D NUCLEIC ACID

<400> 81

gagttcgacg ggagggtggc caggcaaata gtgtcatcga ttggcctatg tcgttatggt 60  
gggaggattg actgctgctg gggctgggct cgccagtctt ggggacagtg tcagcctgtg 120  
tgccaaccac gatgcaaaca tggggaatgt atcgggcca acaagtgcaa gtgtcatcct 180  
ggttatgctg gaaaaacctg tattcaagtt taaatgagt gtggcctgaa gccccggccc 240  
tgttaagcaca ggtgcatgaa cacttacggc agctacaagt gctactgtct caacggatat 300  
atgctcatgc cggatgggtc ctgctcaagt gccctgacct gctcatggc aaactgtcag 360  
tatggctgtg atgttgtaa aggacaaata cggtgccagt gccatcccc tggcctgcag 420  
ctggctctg atgggaggac ctgtgtgat gttgatgaat gtgtacagg aagagcctcc 480  
tgccctagat ttaggcaatg tgtcaacact ttgggagct acatctgcaa gtgtcataaa 540  
ggcttcgatc tcatgtatat tggaggcaaa tatcaatgtc atgacataga cgaatgtca 600  
cttggtcagt atcagtgcag cagctttgct cgatgttata acgtacgtgg gtctacaag 660  
tgcaaatgta aagaaggata ccagggtgat ggactgactt gtgtgtatat ccaaaaagtt 720  
atgattgaac ctcagggtcc aaltcatgta ccaaaggga atgtaccat tttaaagggt 780  
gacacaggaa ataataattg gattcctgat gtggaagta cttggtggc tccgaagaca 840  
ccatatatc ctctatcat taccaacagg cctacttcta agccaacaac aagacctaca 900  
ccaaagccaa caccaattcc tactccacca ccaccaccac cctgccaac agagctcaga 960  
acacctctac cacctacaac ccagaaagg ccaaccaccg gactgacaac tatagacca 1020  
gctgccagta cacctcagg agggattaca gttgacaaca gggtagagac agaccctcag 1080  
aaaccagag gagatgtgtt cattccacgg caacctcaa atgacttgt tgaatatatt 1140  
gaaatagaaa gaggagtcag tgcagacgat gaagcaaagg atgatccagg tgttctggtg 1200  
cacagtgtg atttgacca tggactttgt ggaatgatca gggagaaaga caatgacttg 1260  
cactgggaac caatcaggga ccagcagggt ggacaatatc tgacagtgtc ggcagccaaa 1320  
gcccagggg gaaaagctgc acgcttggtg ctacctctg gccgcttat gcattcaggg 1380  
gacctgtgcc tgtcattcag gcacaagggt acggggctgc actctggcac actccaggtg 1440  
tttgtagaa aacacggtgc ccacggagca gccctgtggg gaagaaatgg tggccatggc 1500  
tggaggcaaa cacagatcac cttgcgagg gctgacatca agagcgtcgt cttcaaagg 1560  
gaaaaaaggc gtggtcacac tggggagatt ggattagatg atgtgagctt gaaaaaaggc 1620  
cactgctctg aagaacgc 1638

<210> 82

<211> 546

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TRANSLATION

FROM AMPLIFICATION PRODUCT 16467945.0.88-S261.D

<400> 82

Glu Tyr Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser Ile Gly Leu  
 1 5 10 15  
 Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp Ala Arg Gln  
 20 25 30  
 Ser Trp Gly Gln Cys Gln Pro Val Cys Gln Pro Arg Cys Lys His Gly  
 35 40 45  
 Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro Gly Tyr Ala Gly  
 50 55 60  
 Lys Thr Cys Ile Gln Val Leu Asn Glu Cys Gly Leu Lys Pro Arg Pro  
 65 70 75 80  
 Cys Lys His Arg Cys Met Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys  
 85 90 95  
 Leu Asn Gly Tyr Met Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu  
 100 105 110  
 Thr Cys Ser Met Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly  
 115 120 125  
 Gln Ile Arg Cys Gln Cys Pro Ser Pro Gly Leu Gln Leu Ala Pro Asp  
 130 135 140  
 Gly Arg Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser  
 145 150 155 160  
 Cys Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys  
 165 170 175  
 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr Gln  
 180 185 190  
 Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys Ser Ser  
 195 200 205  
 Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys Lys Cys Lys  
 210 215 220  
 Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr Ile Pro Lys Val  
 225 230 235 240  
 Met Ile Glu Pro Ser Gly Pro Ile His Val Pro Lys Gly Asn Gly Thr  
 245 250 255  
 Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn Trp Ile Pro Asp Val Gly  
 260 265 270  
 Ser Thr Trp Trp Pro Pro Lys Thr Pro Tyr Ile Pro Pro Ile Ile Thr  
 275 280 285

Asn Arg Pro Thr Ser Lys Pro Thr Thr Arg Pro Thr Pro Lys Pro Thr  
290 295 300

Pro Ile Pro Thr Pro Pro Pro Pro Pro Pro Leu Pro Thr Glu Leu Arg  
305 310 315 320

Thr Pro Leu Pro Pro Thr Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr  
325 330 335

Thr Ile Ala Pro Ala Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp  
340 345 350

Asn Arg Val Gln Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ile  
355 360 365

Pro Arg Gln Pro Ser Asn Asp Leu Phe Glu Ile Phe Glu Ile Glu Arg  
370 375 380

Gly Val Ser Ala Asp Asp Glu Ala Lys Asp Asp Pro Gly Val Leu Val  
385 390 395 400

His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu Lys  
405 410 415

Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly Gly Gln  
420 425 430

Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys Ala Ala Arg  
435 440 445

Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly Asp Leu Cys Leu  
450 455 460

Ser Phe Arg His Lys Val Thr Gly Leu His Ser Gly Thr Leu Gln Val  
465 470 475 480

Phe Val Arg Lys His Gly Ala His Gly Ala Ala Leu Trp Gly Arg Asn  
485 490 495

Gly Gly His Gly Trp Arg Gln Thr Gln Ile Thr Leu Arg Gly Ala Asp  
500 505 510

Ile Lys Ser Val Val Phe Lys Gly Glu Lys Arg Arg Gly His Thr Gly  
515 520 525

Glu Ile Gly Leu Asp Asp Val Ser Leu Lys Lys Gly His Cys Ser Glu  
530 535 540

Glu Arg  
545



<210> 83  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 83  
cagtcaatgg gtaccagaaa ataaca 26

<210> 84  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 84  
cctgggctta tcaacggacg cca 23

<210> 85  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 85  
accacggtgc caatttagc 20

<210> 86  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 86  
gctaaatcct gtccatctgt gt 22

<210> 87  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE  
  
<400> 87  
tgaaaccgc atcgagcga 20

<210> 88  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
  
<400> 88  
atggatgtca gaaagcgatc a 21

<210> 89  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
  
<400> 89  
cagtcacaca gctgctctat ttca 25

<210> 90  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE  
  
<400> 90  
aaatctaccc cttgcgtggc tggaac 26

<210> 91  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
  
<400> 91  
ggacacctcc agggaaacgt 20

<210> 92  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 92  
cctgcaaagc cgtgaggt 18

<210> 93  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 93  
acggcatctc tgttgccgga acc 23

<210> 94  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 94  
ggtgtcctgg tagattcgga ag 22

<210> 95  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 95  
gtactgccgc cagcttacct 20

<210> 96  
<211> 28  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PROBE

<400> 96

cacagagcca gcagtgacac atgacaaa

28

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 97

gacatggctt tcgtaaataa tgca

24

<210> 98

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 98

cgcccctaca accgcat

17

<210> 99

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PROBE

<400> 99

ccatagagtc agcgtttgac aatccaactt acg

33

<210> 100

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 100  
ctgcaaagga aagagatcca gtc 23

<210> 101  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 101  
ttggcctgga ctgcttcttc 20

<210> 102  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 102  
catctctgtc taccttggt atggcgtg 28

<210> 103  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 103  
aggctgat tctggacctt gatt 24

<210> 104  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 104  
ccaagtagat gggttctgtt tgc 23

<210> 105

<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 105  
cccagttacc tccacagggt atttcca 28

<210> 106  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 106  
cgacgctgct gctcagtata ac 22

<210> 107  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 107  
ccacctacaa cccagaaag g 21

<210> 108  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 108  
caaccaccgg actgacaact atagcaccag 30

<210> 109  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 109

tgtaatccct cctggagggtg tac

23

<210> 110

<211> 87

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TRANSLATION  
FROM AMPLIFICATION PRODUCT 16467945.0.85-S259.A

<400> 110

Glu Tyr Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser Ile Gly Leu  
1 5 10 15

Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp Ala Arg Gln  
20 25 30

Ser Trp Gly Gln Cys Gln Pro Val Cys Gln Pro Arg Cys Lys His Gly  
35 40 45

Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro Gly Tyr Ala Gly  
50 55 60

Lys Thr Cys Asn Gln Ala Val Gly Phe Glu Arg Cys Met Val Pro Ala  
65 70 75 80

Gly Arg Arg Gly Ser Thr Leu  
85